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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10044205/runat_06082004_104323_23412/app_query.fasta_1.711
-Q=/cgn2 1/USPTO_spool/US10044205/runat_06082004_104323_23412/app_query.fasta_1.711
-DB=Published_Applications_NA -QFMT=fastap_-SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pbc -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10044205 @CGN 1_1_354 @runat_06082004_104323_23412
-NCPU=6 -ICPU=3 -NO_MAAP -LARGEQUERY -NBG_SCORES=0 -WAIT -DSPBLOCK=100
-NCPU=6 -ICPU=3 -NO_MAAP -LARGEQUERY -NBG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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Perfect score:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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gn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
gn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
gn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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ALIGNMENTS

US-10-044-205A-3

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Sequence 3, Application US/10044205A
Publication No. US20020123464A1
GENERAL IMFORMATION:
APPLICANT: KAPELLER-LIBERMANN, Rosana
APPLICANT: KAPELLER-LIBERMANN, Rosana
APPLICANT: KAPELLER-LIBERMANN, Rosana
APPLICANT: Warnion: Bood, 15821, and 15418, Methods and Compositions of Human Proteir
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 10147-5201
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR APPLICATION NUMBER: US 60/241,884
PRIOR APPLICATION NUMBER: US 60/241,887
PRIOR APPLICATION NUMBER: US 60/241,877
PRIOR TILING DATE: 2000-10-20
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
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Result No.

Score

Query Match Length DB

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Description

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Percent Similarity:
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                                         LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle
                                                                                               GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer
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RESULT US-10-0 ; Seque	Db	Qy	Db	Ş	Db	8	Db	Ą	ДЪ	δ	뫄	Ş	Дb	8	DЪ	VQ	Db	Ş	Db	VΩ	Db	γQ	DЪ	γQ	DЬ	VQ
SULT 2 -10-044-205A-1 Sequence 1, Application US/10044205A	1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659	541 GluGlyAsnSerSerLySSerGlyValCysLeuLeuLeu 553	1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540	1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520	1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500	481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500	1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1440	461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480	1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380	441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460	1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320	421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440	1201 GAGGATCTGAAGGAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260	401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420	1141 ATTTATGAAATGGTTGGTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200	381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400	1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140	361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380	1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080	341 MetLysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360	961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020	321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340	901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960	301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysDroGlu 320

; sequence 1, Application US/10044205A
; bublication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: BAIDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of H
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1

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Best Local Similarity:
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GENERAL INFORMATION:

APPLICANT: Walke, D. Wade

APPLICANT: Wilganowski, Nathaniel L.

TITLE OF INVENTION: No. US20030004328A1el Hu

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: LEX-0147-USA

CURRENT APPLICATION NUMBER: US/10/217,745

CURRENT FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: US/09/802,117

PRIOR FILING DATE: 2003-08

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASCEQ for Windows Version 4.0

SEQ ID NO 1
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GANDHI, Ameena R.
TRIBOULEY, Catherine M
CHAMLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
RAMKUMAR, Jayalaxmi
                                                                                                 BANDMAN, Olga
BOROWSKY, Mark L.
AU-YOUNG, Janice
LU, Yan
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ORANIES: Homo sapiens ORANIES: Homo sapiens ORANIES: Misc feature OTHER INFORMATION: Incyte ID No. UB20040023242A1 7477204CB1 US-10-311-034-45 US-10-311-034-45 OTHER INFORMATION: Incyte ID No. UB20040023242A1 7477204CB1 US-10-311-034-45 OTHER INFORMATION: Incyte ID No. UB20040023242A1 7477204CB1 US-10-314-034-45 OTHER INFORMATION: Incyte ID No. UB20040023242A1 7477204CB1 OTHER INFORMATION: Incyte ID No. UB20040023242A1 7477204CB1 US-10-34-45 OTHER INFORMATION: Incyte ID No. UB20040023242A1 7477204CB1 OTHER INFORMATION: Incote ID No. UB20040023242A1 7477204CB1 OTHER INFORMATION: Inco	APPLICANT: GRIFFIN, Jennifer A. APPLICANT: KEARNEY, Liam APPLICANT: BURFORD, Neil APPLICANT: BURFORD, Neil APPLICANT: TANG, Y. Tom APPLICANT: HE, Ann APPLICANT: HE, Ann APPLICANT: HEALTA, April APPLICANT: THORNTON, Michael APPLICANT: GRURDAJAN, Rajagopal APPLICANT: GRURDAJAN, Rajagopal APPLICANT: GRURDAJAN, Rajagopal APPLICANT: GRURDAJAN, Rajagopal APPLICANT: BURFON, Shirley A. APPLICANT: BURGAL, Yalda APPLICANT: BURGAL, Yalda APPLICANT: GRETHER, Megan APPLICANT: GRETHER, Megan APPLICANT: GRETHER, Mesan APPLICANT: GRETHER, Mesan APPLICANT: GRETHER, Mesan APPLICANT: GROW, Craig H. APPLICANT: THANGAVELU, Kavitha APPLICANT: HOWAN KINASES FILE REFERENCE: PT-0125 PCT CURRENT APPLICATION NUMBER: 60/212,073; 60/215,651; 60/216,605; 60/218,372; 60/223,056 PRIOR APPLICANTON NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,372; 60/223,056 PRIOR PILING DATE: 2002-12-10 PRIOR PILING DATE: 2000-06-15; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-07; 2000-07-
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	ACCAAAGACAGCGCCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG AssnProGlnProPheLeuSerglnAlaValAlaThrIvsCysGlnAlaValAlaThrThrGlu AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCAACCACTGAG GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu

; TYPE: DNA ; ORGANISM: Homo sapiens US-10-451-168-49 Alignment Scores:	PRIOR APPLICATION NUMBER: 60/260,482 PRIOR FILING DATE: 2001-01-09 PRIOR APPLICATION NUMBER: 60/264,922 PRIOR APPLICATION NUMBER: 60/264,922 PRIOR APPLICATION NUMBER: 60/266,797 PRIOR FILING DATE: 2001-01-30 PRIOR PILING DATE: 2001-02-06 PRIOR APPLICATION NUMBER: 60/276,988 PRIOR FILING DATE: 2001-03-19 PRIOR FILING DATE: 2001-03-19 PRIOR PILICATION NUMBER: 60/281,535 PRIOR FILING DATE: 2001-04-04 PRIOR APPLICATION NUMBER: 60/289,622 PRIOR FILING DATE: 2002-06-28 NUMBER: OF SEQ ID NOS: 110 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 49 LENGTH: 1662	SSM COOFFICE	Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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301 AlaCysGlyMetLeuHisGluLeuGlyTleValTyrArgAspMetLysProGlu 320	LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys	361 ÁACCCGCÁÁCCCTTCCAGCCÁGCCÁGGCCÁCCÁAGCAAGCAGCAÁGCÁGCAÁCCÁCCÁCCÁCCÁCCÁCCÁCCÁCCÁCCÁCCÁCCÁCCÁC	41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60

Oy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40 Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40	-10-044-205A-2 (1-553) x US-10-217-745-5 (1-2249) 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg	Percent Similarity: 99.82% Conservative: 0 Best Local Similarity: 99.82% Mismatches: 1 Query Match: 99.79% Indels: 0 DB: 15 Gaps: 0	Length: 2883.00 Matches:	; IXE: UNA ; ORGANISM: homo sapiens US-10-217-745-5	SOFTMARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 2249	ILING DATE: LICATION NUMB LICATION NUMB LICATION NUMB LICATION NUMB LICATION NO.	OF INVENTION: Polymucleotides OF INVENTION: Encoding the Same BERBENCE: LEX-0147-USA	APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Turner, C. Alexander Jr. APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: No. US20030004328A1el Human G-Counled Protein Recentor Kinases and	US-10-217-745-5 US-10-217-745-5; Publication US/10217745 ; Publication No. US20030004328A1 ; Publication No. US20030004328A1	۳. س	5-1 TELLEGIUILIGIY HEDERGUIGI UNCUMCHASHASDI III	1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA		1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 481 IVSAsnllaalaGlullassnaheSetGluValatoVValGlubbeAetAaniva	Cy 441 SerArgGluLysserAspAspProArgLysLisHisPhePheLysThrIleAspPhePro 460	421 GAUGARAFAN SKEPT ECYBAR GLEUR ELEURAL BYSHYSE ZOCHUG INARGLEUG IY 1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTTGCTAAGAAACCAGAGCAACGCTTAGGA 1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTTGCTAAGAAACCAGAGCAACGCTTAGGA	1201 GAGGATCTGAAGGAAGGAAGTCAAATTCCAGCATGATAACTTCACA
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381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400	IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer	1314 AATGIGCTICTGGATGACCTCGGCAACTGGAGGTTATCTGACCTGGGGCTGGCCGTGGAGGTGAGCTAGCT	AsnValleuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu	301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320 	281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnTle 300 	261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisTle 280	241 GluileLeuGluLysValSerSerProPheileValSerLeuAlaTyrAlaPheGluSer 260	221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyGluLysMetAlaLeuLeuGluLys 240	201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220	181 PheGluMetGlnProValserAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200 	161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysFheLeuGlnTrpLysLeu 180 	141 GluGluArgValAlaAiaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160 	121 ASnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140	101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120	81 ArgiysAlaAlaThrPheieuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100 	61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80 	41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60

401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420	— У	
1141 ATTTATGAAATGGTTGGTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200	Db	
381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400	Qy	rAspCvsAspSerIvsGluI.euGlpArgArgArgArgSerI.eu
361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhcAlaMetGlyCysSer 380	ου Oy	1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg
ATGAAGGGTGGCAAGCCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG	Db	x US-09-964-469-1 (1-1662)
341 MetLysGlyGyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360	Qy	99.64% Mismatches: 99.55% Indels:
321 ASNVAlLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340 	Qy Db	0 2876.00 Y: 99.648
901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960	D Q	US-09-964-469-1
TyrAssIValGlyThrArgGlyLenAspMetSezArgValllePheTyrSezAlaGlnIle	, B, &	. w H
261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280 	Qy Db	PRIOR FILING DATE: 2000-06-01 PRIOR APPLICATION NUMBER: 09/738,894 PRIOR FILING DATE: 2000-12-18 NUMBER OF SEQ ID NOS: 4
241 GluileLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260 	Qy	REFERENCE: CLOOK NT APPLICATION N NT FILING DATE: APPLICATION NIM
221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyGluLysMetAlaLeuLeuGluLys 240 	Db Qy	APPLICANT: GUEGLER, Karl et al , TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC , TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF
201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220 	Qy Db	US-09-964-469-1 US-09-964-469-1 ; Sequence 1, Application US/09964469 ; Patent No. US20020034803A1 ; GRNERAL INFORMATION:
181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200 	Qy db	
161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180 	עץ סט	
141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160 	Qу	
121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140 	Qy Db	
101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120	dg VQ	
81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100	Qy Db	
61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80	Qγ	
41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60 	Qy Db	

US-10-044-205A-2 (1-553) x US-10-425-962-1 (1-1662). Qy	() []	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 1 ; LENGTH: 1662 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-425-962-1 Alignment Scores.	CURRENT FILING DATE: 2003-04-30 PRIOR APPLICATION NUMBER: 09/964,469 PRIOR FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 09/738,894 PRIOR FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: 60/208,331 PRIOR FILING DATE: 2000-06-01 NUMBER OF SEO ID NOS: 4 NUMBER OF SEO ID NOS: 4	; Publication No. US20030180786A1 ; GENERAL INFORMATION: ; APPLICANT: GUEGLER, Karl et al ; TITLE OF INVENTION: ISOLATED HUMAN KIMASE PROTEINS, NUCLEIC ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KIMASE PROTEINS, AND USES ; TITLE OF INVENTION: THEREOF; ; FILE REFERENCE: CL000636DIV2 ; CURRENT APPLICATION NUMBER: US/10/425,962	RESULT 8 US-10-425-962-1 ; Sequence 1, Application US/10425962	1	501 ASPLYSGIPPHEPHELYSASRPHAPIATTHYGIAPATHYGIA		Qy 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460	
361 IleLeuMetGluLysValSerTyrSerTyrProValAspTTpPheAlaMetGlyCysSer	Qy 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340	Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300	Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260	Qy 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220	Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200	Db 421 GAAGAGCGAGTGGCCGAAGGCAAGGCCTTCTACGAAGATTTCTGCAAGAG 480 Qy 161 GlnProPheLysaspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180 [Qy 121 ASDPTOGINPTOPHELEUSETGINAlaValAlaThrTySCYSGINAlaAlaThrThrGlu 140	241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGAGCTGGCCCAGGAGGACCC 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	Qy 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80	Db 61 AAGCCCTCGGACTGCGACAGGAAAGAGCTGCAGGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120 Oy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60

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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
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US-10-072-012-273
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
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Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
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Shimkets, Richard
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David W.
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Best Local Similarity:
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; ORGANISM: Homo
US-10-072-012-273
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SEQ ID NO 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILLING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-07
PRIOR PILLING DATE: 2001-02-08
PRIOR PILLING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
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GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys
                                                                                                                                                    GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
                                                                                                                                                                                                                            GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu
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                                                                          PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
                                                                                                                                                                                                     GAAGAGCGAGTGGCTGCAGTGACGCTGGCCCAAGGCTGAGGCCCATGGCTTTCTTGCCAAGAG
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                                                                                                                               CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC
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                                                        TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT
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Db RESULT US-10-	S B S	Db Qy	Db VQ	B &	Db Qy	D 29	Db Qy	Ωy	Db Oy	DD QQ	Db Qy	Qy db	99 Vy	Db Qy	B 8	B &	Db
Db 1624 TGTGAGGAGGGTAATTCATCCAAGTCTGCGTGTTTTGTTATTG 1668 RESULT 10 US-10-217-745-3 ; Sequence 3, Application US/10217745	519 GluGluIleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGly 538	499 AspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGln 518 	479 TyralaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAsp 498 	459 PheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValVal 478	440 GlySerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsn 458	13	400 LysGluAspLeuLysGluArgThrLeuGluAspGluValLysPheGluHisAspAsnPhe 419			341 MetLysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaPro 359	321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340 	301 AlaCysGlyMetLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320 	281 TyrasnValGlyThrArgGlyLeuAspMetSerArgValllePheTyrSerAlaGlnIle 300 	261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280 	241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260 	221 LysLeuAspLysLysArgLeuLysLysLysGLYGLYSLULysMetAlaLeuLeuGlutys 240	GGTTTTGGGGAGGTAAAAAACACTGGGAAGATGTATGCCTGTAAG
\$ B \$	Db Qy	D Qy	η γ	\$ &	90 VQ	A 4d	dg VQ	B &	D Qy	Query DB: US-10-	Pred. Score: Percen Best L) US-1	SE		 Сынн	 HDDD	; GE
181 PheGluMetGlnProValSerAspLysTyrPheThrGlubheArgValLeuGlyLysGly 200	GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu	141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160	121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140	101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120 	81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100 	61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80	41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnDheHisSerLeuCys 60 	21 LysproSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40	1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20 	Match: 62.34% Indels: 15 Gaps: .044-205A-2 (1-553) x US-10-217-745-3 (1-1062)	Pred. No.: 2.44e-215 Length: 1062 Score: 1801.00 Matches: 349 Percent Similarity: 99.71% Conservative: 0 Best Local Similarity: 99.71% Mismatches: 1) ORGANISM: homo sapiens US-10-217-745-3	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 1062 ; TYPE: DNA	002-0 R: US	NON PO	APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases	Publication No. US20030004328A1 ENERALA INFORMATION:

Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40	2076 AIGGIGGACAIGGGGCCCIGGACACCIGAICGCCAACACCIGCAGGCCCGG 2135	DINPHILIANCE TO THE CONTRACT OF THE CONTRACT O	Valaenher Clvalatenaenten talahan numberatan murtan Christian	-044-205A-2 (1-553) x US-09-964-46	52.89% Indels:	t Similarity: 41.40% Conservative: ocal Similarity: 41.40% Mismatches:		Alignment Scores:	; OTHER INFORMATION: n = A,T,C or G US-09-964-469-3				SOFTWARE: FastSEQ for SEQ ID NO 3	PRIOR FILING DATE: 2000-12-18 NUMBER OF SEQ ID NOS: 4	PRIOR FILING DATE: 2000-06-01 PRIOR APPLICATION NUMBER: 09/738.894	CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 60/208,331	FILE REFERENCE: CL000 CURRENT APPLICATION N	TITLE OF INVENTION: THEREOF	APPLICANT: GUEGLER, Karl et al	; Sequence 3, Application US/09964469 ; Patent No. US20020034803A1 ; GENERAL INFORMATION:	RESULT 11	1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG	341 MetLysGlyGlyLysProIleThrGlnArq 350	Qy 321 AsnValLettletiAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340	901 GC	Qy 301 AlaCysGlyMetLeuHisGeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320	841 TACAACGTGGGCACGCGTGGACATGAGCCGGGTGATCTTTTACTCGGGCCAGATA	Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300	CY 261 LYSTRIHISIEUCYSIEUVALMECSETIEUMECKSINGLYGIJVABDIEULYSEBHEHISIIE 280	721	241 Glu	Symptomic promise and promise	າ ດ
- 1	Q.	뫄	SS.	Ф	γQ	Db	Qy	Db	Q	DЬ	Qγ	Дb	Оy	Дb	Q	DЪ	Ş	Db	Q	Db Qy	рb	Qy	Db	Qy	g 4	, E	; 8	рь	Ş	당 왕	DЬ	Qy	DЬ
	204	3156 AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCAAAAAAAA	204 204	3096 ACTTGGGAGGCTGAAGCAGGAGAATCACTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCC 3155	204 204	3036 TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGCT 3095	204 204	2976 TGTGTGACAGAAGATCTCCGTTTCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA 3035	204 204	2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA 2975	204 204	2856 TGAAATAAAACACAAATGGCATGAGAGAGACAAGCAAAATTTATACTTGGCCAAGACTCT 2915	204 204	2796 CATAIGIGGAGGATITCIAGCCCCGICTCCCCAGCCCCCTTCTITGIGIGCGAIGGIG 2855	204 204	2736 AAGGGGGTAATGTTGCCTTTCTTTTTAAATCTCAGTTACTTAGAACTAATTTCAGCAC 2795	204 204		201 GlyPheGlyGlu 204	181 PheGluMetGlnProValSerAspLysTyrPheThrGlubheArgValLeuGlyLysGly 200 	CAGC	161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180	2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555	GluGluArgValAlaAlaValThrLeuArgLygAlaGluAlaMetAlapheLeuGlnGlu	121 ASDETGLIPTOPHALAUSATGLIAN AVALANATHTLYSCYSGLIAN ABALATHTINGU 140	ACCAARGACAGCGCTGCAGGGCTGGTCGCCACTTGTGCGAGTGCCCCTGCCCCGGGG	ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	2316 GCCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGTGGCCGAGGAGGAGGACCC 2375	/sAlaAlaThrPheLeuCluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro	61 GluGlnGlnProlleGlyArgArgLeubheArgAspPheLeuAlaThrValBroThrPhe 80	2196 GGGCTGCAGGGGTGCGCGGAGATCCCCCAGAAACCTGCCCTGAAACTTCCACAGCCTGTGT 2255	41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60	2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCCGCGCGCG

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4116 CAGTACCATCTACTTCTACCTCTTTCTCTTTTCTTCTTTTTCTCCTTTAAGGTATGTCCCTT 4175 208 IGINVALLYSASNTHTGIYLYSMEETTYTAIACYSLYSLYSLEUASPLYSLYSATGLEULY 228	AGGAGTATCGCACTGTAGTCCCCACTTTTTCTTGAGAACACTTCTTATT CTTTCTCCAATGCCTAACATCTTTCCACCCACCTCCTCCTTTATCATCT	CCAAACTITCCACATTITTTATTCCCACCAGCAATGCTTAAAGGTTTCGATTTCTCCACA TCCTTGCCAACACTTGATATTTTCCTGTATTTTTTATGAAGGCCTGCCT	3696 TAGCCATTCATCTGTTGATGGACACTTGGGCTGTTTCACCTTTTGGCTATTGTGTATGG 3755 204	204 204 3516 TITCTGTCTCTAGGGATTTGCCTATTCTGGGTGTTTCACACAATATGTGACCTTTTGTGT 3575 204	3216 AAGAAAGAAAGAAAAGAAAACACTTATCTTGAAGTAAAGTTAAGGTTGAGAACCTGTTTTGT 3275 204
US-10-044-205A-2 (1-553) x US-10-425-962-3 (1-36651) Qy	Alignment Scores: 1.32e-178 Length: 3651 Score: 1.528.00 Matches: 349 Percent Similarity: 41.40% Conservative: 0 Best Local Similarity: 41.40% Mismatches: 1 Query Match: 52.89% Indels: 493 DB: 15 Gaps: 1	; SEQ ID NO 3 ; LENGTH: 36651 ; TYPE: DNA ; ORGANISM: Homo sapiens ; PEATURE: ; PEATURE: ; NAME/KEY: misc_feature ; LOCATION: (1) (36651) ; OTHER INFORMATION: n = A,T,C or G US-10-425-962-3	CURRENT PAIRLING DATE: 2003-04-30 PRIOR APPLICATION NUMBER: 09/964,469 PRIOR APPLICATION NUMBER: 09/964,469 PRIOR APPLICATION NUMBER: 09/964,469 PRIOR APPLICATION NUMBER: 09/9738,894 PRIOR PILING DATE: 2000-12-18 PRIOR PILING DATE: 2000-12-18 PRIOR PILING DATE: 2000-06-01 PRIOR PILING DATE: 2000-06-01 NUMBER OF SEQ ID NOS: 4 SOPTWARE: FastSEQ for Windows Version 4.0	Oy 348 rGlhArg 350 Db 4596 CCAGAGG 4602 RESULT 12 US-10-425-962-3 ; Sequence 3, Application US/10425962 ; Publication No. US20030180786A1 ; GENERAL INFORMATION: Axr1 et al ; APPLICANT: GUUGGLER, Xar1 et al ; APPLICANT OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES ; TITLE OF INVENTION: THEREOF ; FILE REFERENCE: CL000636DIV2	268 tserieum

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ACCACIGITGIGCCCAG		aagaaagaaagaaagaaagaaacacttatcttgaagtaaggttgagaacctgttttgt		aagatcgtgccactgcactccagcctgggtgacagagcaagactcaaaaaaaa		ACTTGGGAGGCTGAAGCAGGAGAATCACTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCC		TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGCT		TGTGTGACAGAAGATCTCCGTTTCCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA		GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA		TGAAATAAAACACAAATGGCATGAGAGAGACAAGCAAAATTTATACTTGGCCAAGACTCT		CATATGTGGAGGATTTCTAGCCCCGTCTCCCCAGCCCCCTTCTTTGTGTGTG		AAGGGGGTAATGTTGCCTTTCTTTTTTAAATCTCAGTTACTTAGAACTAATTT		 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCATAGAGCATGA	GlyPheGlyGlu	TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAAGGT	PheGluMetGlnProVa		GlnProPheLvsAsnPh	 PAGAGCO	GluGluArqValAlaAl	AACCCGCAACCCTTCCT	AsnProGlnProPheLe		ThrLysAspSerAlaLe	CGCAAGGCGGCAACCTT	drafire [selections	GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe
CTG11G1GCCCAGCT11C1G11T1TAAGTAATAAAATTATTTCAGGTAAAATTTG		AGAAAACACTTATCTTG		TCCAGCCTGGGTGACAG		GGAGAATCACTTGAGCC		CTCTAACTAGCTGGGTG		CGTTTCCCCTAAATTGT		KAACGTGCTGAGATGCC		; GCATGAGAGAGACAAGO		PAGCCCCGTCTCCCCAGC		TTCTTTTTTAAATCTO		rgtctcccagtagccago			lSerAspLysTyrPheTh	GTGACCAGCGCCTTCT	ValThrSerAlaPheTy		aValThrLeuArgLvgAl		ıSerGlnAlaValAlaTl		ıGlnGlvLeuValAlaTl	SALGALA LILE FILEMEN LIMB PRATATION TO THE PROPERTY OF THE P		VArgArgLeuPheArgA
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288 uAspl	4356 GAGC	268	248 rPro	4236 GAAG	228 sLys	4176 CCAG	208 1Gln	4116 CAGT	Qy 205	4056 CTTT	204	3996 AGGA	204	3936 TCCT	Qy 204	3876 CCAA	Оу 204	3816 GCCC	Qу 204	3756	Qy 204	3696	Qу 204	3636	Qу 204	3576	Qy 204	3516	Qy 204	3456	Qy 204	3396	Qy 204	3336
288 uAspl	4356 GAGC	268	248 rPro	4236 GAAG	228 sLys	4176 CCAG	208 1Gln	4116 CAGT	205	4056 CTTT	204	3996 AGGA	204	3936 TCCT	204	3876 CCAA	204	3816 GCCC	204	3756		3696	204	3636		3576		3516		3456	204	3396		3336
288 uAspl	4356 GAGC	268	248 rPro	4236 GAAG	228 sLys	4176 CCAG	208 1Gln	4116 CAGT	205	4056 CTTT	204	3996 AGGA	204	3936 TCCT	204	3876 CCAA	204	3816 GCCC	204	3756		3696	204	3636		3576		3516		3456	204	3396		3336
	4356	268	•	4236 GAAG	228 sLysI	4176 CCAG	208 1Gln	4116 CAGT	205	4056	204	3996	204	3936	204	3876	204	3816	204	375		t.i	204					W		345	204	tu		333

Sequence 2, 30-2 Sequence 2, 30-2 Publication No. UB2003015352A1 SERBAL INFORMATION: UB2003015352A1 SERBAL INFORMATION: UB20030153CA1 SEPICARY: Millennium Pharmaceuticals, Inc APPLICARY:	Qy 348 rGlnArg 350 Db 4596 CCAGAGG 4602 RESULT 13	328 yAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleTh 	Db 4416 GGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCA 4475 Qy 308 sGluLeuGly1leValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGl 328
B	QY QQ QQ	Qy	Db Qy Db
197 LeuiclyLysolydlyPhodlyCluvalCysalavalGanacAccarTTAGACACTTAGAGGT 576 197 LeuiclyLysolydlyPhodlyCluvalCysalavalGlnvalLysAsmThrOlyLysMet 216 297 TYZAlaCysLysLysLysLeuispLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysGlyGlyGluLysMetAla 236 217 TYZAlaCysLysLysLysLeuispLysLysLysLysLysGlyGlyGluLysMetAla 236 218 LeuiswlalayCluLysLawAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176	.43 ArgVa:	307 CTGTCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCCTTTACCAGAAATACCT 366 123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142

PILE REFERENCE, MPIO1-294PIRMW CURRENT FILING DATE: 2002-12-19 PRIOR APPLICATION NUMBER: US 60/341,953 PRIOR APPLICATION NUMBER: US 60/341,953 PRIOR PELICATION NUMBER: US 60/341,953 PRIOR REPLICATION NUMBER: US 60/341,953 PRIOR PELICATION NUMBER: US 65.494 PRIOR PELICATION NUMBER: US 60/341,953 PRIOR PELI	Qy 476 SerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyVal 495 Db 1411 CATGCCGTTTACTGTAAGGACGTCCTGGATATCGAGAGTTCTCGGCGTGAAAGGATC 1470 Qy 496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
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951 CHAANGAMAGAATTCHGAGAAGTGCAAAGTAGATTGGTIGTTAGTTTAGCCTAC 1010 257 AlaPheGluSerLysThrHisteuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276 257 AlaPheGluSerLysThrHisteuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276 257 EysPheHistleTyrAsnValGlyThrATGGTGTGTGTCCCCCTTTATTAATGGAGGGATTTG 1070 277 LysPheHistleTyrAsnValGlyThrATGGILLeuWisgGluLeuGlyTleValTyrArgAsp 316 277 EysPheHistleTyrAsnValGlyThrATGGGTGTTGATGAGGAGAAGAAGATTTGATGAGGAGATTTG 1070 277 LysPheGluGartaAAGATGCCTTGGGCATTGATGAGAAGAAGAAGAGCCGTTTTCTAHT 1130 278 SerAlaGln11eAlaCysGlyMetLeuHistLeuHisGluLeuGlyTleValTyrArgAsp 316 279 SerAlaGln11eAlaCysGlyMetLeuHistLeuHisGluLeuGlyTleValTyrArgAsp 316 271 HistlySProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspCAGAGCCGTTTTCTAHT 1130 277 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspCAGAGAGCTCGGGT 1250 317 MetLysProGluAsnValTeuLeuAspAspLeuGlyAsnCysArgLeuSerAspCAGAGAGCTCGGGT 1250 318 TTGAGGCTGAGAATTCCCAAAAGACAGAGGTCTGAGAAGAAGAGATTCAGAACATTCCAGAAAGAGATTCCAGAAAGAA	621 CCAGAT

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SOFTWARE: PERL Program
SEQ ID NO 110
LENGTH: 2467
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APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN
FILE REFERENCE: PA-0046 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Susan Stuart
APPLICANT: Jed G. Nucht
APPLICANT: Sharon E. P.
APPLICANT: Jason M. Sh
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CURRENT FILING DATE: 2002-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature OTHER INFORMATION: Incyte ID
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            464 AAGTCCCCTGTTTTCATAGCCCAAGTTGGCCAAGACCTGGTCTCCCAGACGGAGGAGAAG
                                            120 GlyAsnPro----
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                                                                                                                                                                      GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
                                                                                                                                                                                                                                                                          GAAGACCTCCGAAGGACCATAGACAGAGATTACTGCAGTTTATGTGACAAGCAGCCAATC
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                                                                                                                                                                                                            GGGAGGCTGCTTTTCCGGCAGTTTTGTGAAACCAGGCCTGGGCTGGAGTGTTACATTCAG 373
                                                                                                        ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
                                                                                                                                            TTCCTGGACTCCGTGGCAGAATATGAAGTTACTCCAGATGAAAAACTGGGAGAGAAAGGG 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValTyrhrgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
ValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGly 511
                                                             ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu
                                                                                                                         HisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProPhe
                                                                                                                                                                 AAAGATGCGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGGCTGCAGAGGTCAAGAGACAC
                                                                                                                                                                                       LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
                                                                                                                                                                                                                                 GTGTACTCCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACG
                                                                                                                                                                                                                                                            LysPheGlnHisAspAsnPheThrGluGluAlaLysAspTleCysArgLeuPheLeuAla 432
                                                                                                                                                                                                                                                                                                GGCCGCAAGGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAG
                                                                                                                                                                                                                                                                                                                                                              ACTGTTGGCTACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCC 1225
                                GTTCCAGACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACT 1582
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Sear Job	ф	ΔÃ	В	Ş	Дb	Ş	Дb
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Search completed: A Job time : 573 secs	1763	535	1703	532	1643	512	1583
Search completed: August 13, 2004, 21:21:52 Job time : 573 secs	1763 CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGCAGC 1802	535 gProThrGlyCysGluGluGlyAsnSerSerLysSer 547	1703 GTGTTTGGACCTAATGGTACCCTCCCGCCAGATCTGAACAGAAACCACCCTCCGGAACCG 1762	532AspPro-AspAr 535	1643 TCTGTGTCCATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAAC 1702	512 AlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531	:::

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Minimum DB
Maximum DB
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=(pgn2_1/USPTO_spool/US10044205/runat_06082004_104322_23357/app_query.fasta_1.711
-Q=(pgn2_1/USPTO_spool/US10044205/runat_06082004_104322_23357/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rg= -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USERS-US10044205_@CGN 1 1_2568 @runat_06082004_104322_23357 -NOPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -NGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	81 PheGluMetGlnProValSerAspLysTy	161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180	141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160	121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140	101 ThrLysAepSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120	81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100	61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80	41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60	21 LysProSerAepCysAspSerLysGluLeuGlnArgArgArgArgAerLeuAlaLeuPro 40	1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20	6 Gaps: (1-553) x AX797554 (1-1659)	00.00%	Length: Matches:	db_xref="taxon:9606"		Kapeller-Libermann,R. and Bandaru,R. Method and compositions of human proteins and uses thereof Patent: WO 02095032-A 3 28-NOV-2002; MILLENIUM PHARMACEUTICALS, INC. (US)	Homo sapiens Eukaryota; M Mammalia; Eu	Homo sapiens (human)	AX797554	AX797554
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181 Phe 831 TTC 201 Gly 	Qy 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160	Oy 101 ThruysAspSerialenGathGryPenvaladIntCyshadserialerToylar 1001 y 101 ThruysAspSerialenGathGryPenvaladIntCyshadserialerToylar 1001 y 101 AcchangaCagGCGCGCGCGGGGGGGGCCCCGGGGGGGGGGGGG	471 GAGCAGCAGCCATCGGTCGCCGCCTTCCGTGACTCTCTAGCCACAGTGCCCACGTTC 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsmTrpGluLeuAlaGluGluGlyPro	41 GlyL 411 GGGC 61 GluG	291 21 351	Mismatches: Indels: Gaps: 7552 (1-2198)	1.01e-250 2889.00 100.00%	source 1. 2190 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN	Kapeller-Lib Method and c Patent: WO O MILLENIUM PH	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	LOCUS AX797552 2198 bp DNA linear PAT 04-OCT-2003 DEFINITION Sequence 1 from Patent WO02095032. ACCESSION AX797552 VERSION AX797552.1 GI:37518055 KEYWORDS .
Oy 541 GliGIVARNETSETLYSSETCHY NET UP 1939	1791 ASUM ASUM	1671 CCCC 481 Lysa 1731 AAAG	Db 1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAAAAACCAGAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAACAA	GluaspleutyscinArgThrieucinAspGluvaLusyrhecinHishShapasirieinE	1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGAATGAAGC 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys	341 MetLysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu	321 AsnVa 1251 AATGI	Db 1131 TACAACGTGGCACGCGTGGCCTGGACATGAGCCGGGGTGATCTTTTACTCGGCCCAGATA 1190 Oy 301 AlacysglymetLeuHiscluLeuGlyIleValTyrArgAspMetLysProGlu 320	Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280	Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260	Db 891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950 Oy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyGlyGlyGlySMetAlaLeuLeuGluLys 240

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Walke,D.W., Wilganowski,N.L. and Turner,C.A.
Human G-coupled protein receptor kinases and
encoding the same
Patent: US 6444456-A 1 03-SEP-2002;
Location/Qualifiers
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                                                     GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys
                                                                                               TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAAGGT
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Lexicon Genetics Incorporated (US)
Location/Qualifiers
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Human g-coupled protein receptor kinases and polynucleotides
encoding the same
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LysLeuAspLysLysArgLeuLysLysLysGlyGluLysMetAlaLeuLeuGluLys
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                                                                                                     PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly
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Qy 1	Оу 1 Db 4	Qy 1	Qy 1	Qy 1	B 84	Qy Db 1	D 64	Qy Db	Qy Db	DB:	Pred. No.: Score: Percent Sir Best Local	ORIGIN Alignment :		FEATURES source	TITLE		REFERENCE AUTHORS	ONOMINE	KEYWORDS SOURCE
181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200 	61 81	141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160 	121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140 	101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120 	81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100 	61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80	41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60	21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40	1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20	Gaps:) x AX642968 (1-1662)	Pred. No.: 2.45e-250 Length: 1662 Score: 2883.00 Matches: 552 Percent Similarity: 99.82% Conservative: 0 Best Local Similarity: 99.82% Mismatches: 1 Onerv March: 99.70% Taching Conservation	Scores:	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:966" /note="Incyte ID No: 7477204CB1"	Incyte Ger	Recipon, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M., Elliott, V.S., Thangavelu, K., Batra, S. and Ison, C.H. Humain kinases Patrat No. 21005547 1 (5.00 procon)	Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A., Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N., Nguyen,D.B., Tang,Y.T., Baugh,M.R., He,A., Thornton,M., Hafalia,A. Parteron Greenwalds B. T.	1 Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,	nomo saptens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens (human)
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Qy 1 MetValAspMetGlyAlaLeuAspAsnLeuIeAlaAsnThrAlaTyrLeuGlnAlaArg Qy 2 MetValAspMetGlyAlaLeuAspAsnLeuIeAlaAsnThrAlaTyrLeuGlnAlaArg 2 MetValAspMetGlyAlaLeuAspAsnLeuIeAlaAsnThrAlaTyrLeuGlnAlaArg 2 MetValAspMetGlyAlaLeuAspAsnLeuIeAlaAsnThrAlaTyrLeuGlnAlaArg 2 MetValAspMetGlyAlaLeuAspAsnLeuIeAlaAsnThrAlaTyrLeuGlnAlaArg 2 MetValAspMetGlyAlaLeuAspAsnLeuGlnArgArgArgArgArgArgArgArgArgArgArgArgArgA	ari :	COMMENT OS Homo sapiens (human) PN WO 02103020-A/10 PD 27-DEC-2002 PF 14-JUN-2001 WO 2002JP005942 PF 14-JUN-2001 JP 01D 182554 PI NOBUYUKI KOYAMA, SEITCHI TANIDA, KOJI YAMAMOTO PC C12115/54, C12N9/12, G01N33/50, G01N33/15, C07K16/40, A61K39/395 A novel gene relating to disease and use thereof FH Key Location/Qualifiers FT source 11761 FEATURES 1 Location/Qualifiers FI Location/Qualifiers	RESULT 6 BD186115 LOCUS LOCUS BD186115 DEFINITION A novel gene relating to disease and use thereof. ACCESSION BD186115.1 GI:31878315 VERSION BD186115.1 GI:31878315 VERSION WO 02103020-A/10. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) CRGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1761) REFERENCE 1 (bases 1 to 1761) ROYAMA, N., Tanida, S. and Yamamoto, K. DOURNAL Patent: WO 02103020-A 10 27-DEC-2002; TAKEDA CHEMICAL INDUSTRIES LTD, NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI YAMMAOTO
20 20 20 21	Db 866 TACAACGTGGCACGCTGGACCTGGACCTGGACCTGGACCTTTTTACTCGGCCCAGATA 925 Qy 301 AlaCysGlyMetLeuHisCluLeuGlyIleValTyrArgAspMetLysProGlu 320	Db 686 AAACTGGACAAGAAGCGCTGAAGAAGAAGAAGCTGCGAGAAAGTGGCTCTTTGAAAAG Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer	2y 141 3 Db 446 Oy 161 Db 506 Oy 201 Db 626

Alignment Scores: 2.71e-250 Length: 1799 Pred. No.: 2883.00 Matches: 552 Score: 2883.00 Matches: 552 Percent Similarity: 99.82% Conservative: 0 Best Local Similarity: 99.82% Mismatches: 1 Query Match: 99.79% Indels: 0 DB: 99.79% Gaps: 0 US-10-044-205A-2 (1-553) x AF439409 (1-1799)	KFHINNOGREIGLÖMSKVI FYSAQI ACÇMHILHELGI VENKH KFESKI HULUNGSLEMNGUD KFHI INNOGREIGLÖMSKVI FYSAQI ACÇMHILHELGI VERBIKÇEMK CENULLDDIGANCELSD LGALAVEMKOGKE TÖRAĞING YAMPETLIMEKUSYSY PUDWERMGGSI YEMVAGRIYEFK DYKEKVISKEDLKORTLODE VERÇÜHDNETEBAKDI CELFILAKKPEQRLGSREKSDDFRK HHFFETTINE PRILAGILE PEPVPDDSVVYAKDI ABILDDFSEVNGVEEDDKOKQEFKNF ATGAVPIAWQEBI I ETGLFBELNDPNRPTGCEBGNSSKSGVCLLL"	/product="G-protein-coupled receptor kinase 7" /protein_id="AAL48216.1" /protein_id="AAL48216.1" /db xref="G1:1793325" /db xref="G1:179325" /db	CDS 138. 1799 /gene="RK7" /codon_start=1	/map="3q21" /tissue_type="retina" /tissue_type="retina" /gene="0RK7"	/c}/dr /mc/ /or/	AL S		Chen, Y.J., Frederick, J.M. and Bachr, W. TITLE Characterization of human GRK7 as a potential cone opsin kinase JOURNAL Mol. Vis. 7, 305-313 (2001) MEDLINE 21626561		AF439	4 ×	Db 1646 GÄGGGTÄÄTTCÄTCCÄÄGTCTGGCGTGTGTTTÄTTG 1684 RESULT 7 AP439409	541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553	Qy 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540	Db 1526 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1585
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Alignment Scores: 2883.00 Pred. No.: 2883.00 Matches: 552 Percent Similarity: 99.82% Percent Similarit	6		Qy 521 IlelleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540	Db 1518 CGCCTGGAAGCTGGCCTAATTGACCCCCATTTGTGCCAGACCCTTCAGTGGTTATGCC 1577 Qy 481 LysasplealaGluIleaspaspPheSerGluValargGlyValGluPheAspAspLys 500	Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440	Qy 361 IleLeuMetGluLysValSerTyrBerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Osawa, S. and Weiss, E
Direct Submission
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 3186)
                                                                                                                                                                                                                                                and Weiss, E.R.
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G protein-coupled :
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receptor kinase 7 m
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HPERTTINEDRIF ANT IRDRUNDFUNDATAY DE IN TONGGENGCUNDENK

260	GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer	Qy 241	_
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220 744	GIYEREGIYGINVALLYSALAVALGINVALLYSASTTRTGIYIYSMETTYTALACYSIYS	Db 685	н ~
684	TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT	- . o	
200	PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly	Qy 181	~
624	CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAAACTC	Db 565	_
180	GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu	Qy 161	_
564	GAAGAGCGAGTGCCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG	(n	_
160	GluGluArqValAlaAlaValThrLeuArqLvsAlaGluAlaMetAlaPheLeuGlnGlu		_
504 6	ACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACTGCCAAGCCAAGCCACCACCACTGAG		
3.0	AspDroGlpDroDhereiserGlpAlaValaTalaThriveCveGlpAlaThrThrClv	0v 121	_
120 444	ThrIysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	Qy 101 Db 385	
384		(LJ	_
0	ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlvPro	Qy 81	_
80 324	GludinGinProiledlyArgArgieuPheArgAspPheieuAlaThrValProThrPhe	Oy 61 Db 265	
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	A-2 (1-553) x AF282269 (1-3186)	US-10-044-205A	
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                                                                                                                                                                           GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu
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Guegler, K., Beasley, B.M. and Di Francesco, V.
Isolated human kinase proteins, nucleic acid
human kinase proteins, and uses thereof
Patent: US 6331423-A 1 18-DEC-2001;
Coation/Qualifiers
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                               GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer
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                                                                                                                                                                                          TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT
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                                                                        AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAAG
                                                                                                                                  GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG
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AR343544
AR343544.1 GI:3
Unclassified.

1 (bases 1 to 1662)

Guegler, K., Beasley, E.M. and Di Francesco, V.
Isolated human kinase proteins, nucleic acid molecules
                                                         Unknown
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                                                     LysLeuAspLysLysArgLeuLysLysGlyGlyGlyGluLysMetAlaLeuLeuGluLys
 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC
               LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle
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Sequence 1 from Patent WO0192496.
AX357902
AX357902.1 GI:18674690
Guegler, K., di Francesco, V. and Beasley, E.M. Isolated human kinase proteins, mucleic acid human kinase proteins, and uses thereof patent: WO 0192496-A 1 06-DEC-2001;
                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                             Homo sapiens (human)
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             AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC
                                        LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle
                                                                                                GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
                                                                                                                         <u>AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAA</u>
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REFERENCE

AUTHORS TITLE JOURNAL

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RESULT 15 AX166511 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE TOURNAL	B	. B
AX166511 Sequence 2 from Patent WO0138503. AX166511 AX166511 GI:14546856 . Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clary,D.S. Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 2 31-MAY-2001;	841 TÄCÄÄČGTGGGCTGAÄCTTGGAČCTGGÄCCTGÄÄCTTTTTTCTTGGCCCAAATTA 900 301 AlaCyselyMet_LeuHiscaluLeuGlyIleValTyTAtgAspNetLyssProGlu 320 901 GCCTGTGGGATCTGGACCTCCTGAACTTGGCACCTGATTATTGGCACCTGTATGGCCCAAATTA 900 321 ASTVALLeuLeuAspAspLeuGlyAsmCysArgLeuSerAspLeuGlyLeuAlaValGlu 340 961 AATGTGCTTGGATCTGGACCTGGCACTCCGGGTATTGTGATCGGCACCTGAGG 960 321 ASTVALLeuLeuAspAspLeuGlyAsmCysArgLeuSerAspLeuGlyLeuAlaValGlu 340 961 AATGTGCTTGGATCACCCACGGATATTCGACCTGAGGTTATTCCAGCTGGAGTTATTCCAGCTGGAGTTATTCCAGCTGGAGTTTGCCATGCACCTGGGGTAGTTGGCTCCTGGG 1080 341 MetLysslyGlyLyssProlleThrolhAspAlaCCTAAGGATACCAGGTATTCCAGCATCATCCAGGTATCCATGCAGGTACCCTGGGGATGGTATCCATGCTGAGGTCGACCACCTGGGGATGGTATCCATGCATG	281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValllePheTyrSerAlaGlnIle 300
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GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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xrgGlyValGluPheAspAspL :GGGGGTGGAATTTGATGACA
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ysLysProGluGlnArgLeuG AGAAACCAGAGCAACGCTTAA
GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr
IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys
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MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu
AsnValleuleuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu
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TyrAsnValGlyThrArgGlyLeuAspMetSetArgValIlePheTyrSerAlaGlnIle

Search completed: August 13, 2004, 20:25:11 Job time : 4257 secs

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Result
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-G=/Cgn2_1/USPTO_spool/US10044205/runat_06082004_104321_23348/app_query.fasta_1.711
-DB=N_Genesseq_29Jan04_-OpmY=fastap_SUFFIX=p2n.rng_-MINMATCH=0.1_IOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_-OUTFMY=pto -NORM=ext -HEARSIZE=500 -MINIEN=0 -MAXIEN=2000000000
-USER=US10044205_@CGN_1_1_352_@runat_06082004_104321_23348 -NCPU=6 -ICPU=3
-DBY_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG
-NO_MAAP -LARGEQUERY_NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Aad26466 Human kin
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ABS57375 ABS57375 standard; cDNA; 2198 В₽ ALIGNMENTS

cDNA encoding human GPCR kinase (GPCRK) 69087. 04-FEB-2003 (first entry)

ABS57375;

metastatic disorder; cytostatic; gene therapy; gene; ss. Human; G protein coupled receptor kinase; GPCRK 69087; cellular proliferative disorder; differentiative disorder; haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;

Homo sapiens.

THE STATE OF THE S 19-OCT-2000; 2000US-0241884P. 20-OCT-2000; 2000US-0241877P. 22-OCT-2001; 2001US-00044205 US2002123464-A1. CDS /product= "GPCRK 69087"
/note= "The coding sequence given as SEQ ID No:3
specifically claimed in Claim 1" /*tag= Location/Qualifiers

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Best Local Si
Query Match:
DB:
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cu nuclear signalling protein designated 1521, and a novel human mitogen-
cu coupled receptor (GPCR) kinase (MAPKP) phosphatease MAPKP designated 15418, and
cu citivated protein kinase (MAPKP) phosphatease MAPKP designated 15418, and
cu citivated protein kinase (MAPKP) phosphatease MAPKP designated 15418, and
cu citivated protein kinase (MAPKP) phosphatease MAPKP designated 15418, and
cu he polymucleotide sequences encoding them. The sequences such as
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cu cellular proliferative and differentiative disorders (e.g. haematopoietic
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cu disorders). They are also useful in screening assays, detection assays
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cu rials and pharmacogenomics), and in methods of treatment (e.g.
cu cities and pharmacogenomics). The sequences may also be used to screen
cu therapeutic and prophylactic). The sequences may also be used to screen
cu therapeutic and prophylactic). The sequences may also be used to screen
cu the polypeptide sequences are useful as immunogens to generate antibodies
cu mapping their respective genes on a chromosome, identifying gene regions
cu associated with cellular proliferative or differentiative disorders, and
cu associated with cellular proliferative or differentiative disorders, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kapeller-Libermann R,
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The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NHP (novel human protein) in the specification, which is claimed in the invention. The invention comprises protein coupled receptor kinases. Oligonucleotides derived from the screening libraries and assessing gene expression patterns. The nucleotides of the invention are useful as hybridisation probes for nucleotides of the invention are useful as hybridisation probes for nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRK expression. The nucleotides of the products in vivo. The nucleotide sequences of the invention can be used to genetically engineer host cells to express GRK useful in addressable arrays for identifying and characterising the screen collections of genetic material from patients who have a particular medical condition. The proteins of the invention are useful for generating antibodies, as reagents in diagnostic assays, for	New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological disorders. Claim 1; Page 30; 34pp; English.	Walke DW, Wilganowski NL, Turner CA; WPT; 2001-570872/64. P-PSDB; AAG77815.	10-MAR-2000; 2000US-0188449P. (LEXI-) LEXICON GENETICS INC.	08-MAR-2001; 2001WO-US007500.	20-SBP-2001.	W0200168869-A2.	<pre>Key Location/Qualifiers CDS 11662 /*tag= a /product= "G-protein coupled receptor kinase 1"</pre>	Homo sapiens.	G-protein coupled receptor kinase; GRK; human; drug screening; gene expression characterisation novel human protein.	3 Human G-protein coupled receptor kinase 1 cDNA sequence.	T 08-MAR-2002 (first entry)	C AAH78797;	RESULT 2 RAH78797 ID AAH78797 standard; cDNA; 1662 BP. XX	_	1851 541	521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspÞroAsnArgÞroThrGlyCysGlu	Db 1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1ec	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identifying other cellular gene products related to GRK, in assays for screening for compounds that are useful in mental, biological or medical disorders/diseases
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                                   wound healing disorders; atherosclerosis; Parkinson's disease;
Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
inflammation; neoplastic disease; nervous system disorder;
                                                                                                                                                                                              Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
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cardiovascular disorders; pancreatitis; respiratory disorder;
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30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0281535P.
08-MAY-2001; 2001US-0289622P.
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Secreted proteins and polymucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, parkinson's disease, Alzheimer's disease, infection, autoimmune disorder wounds, atheroscierosis, infection, autoimmune disorder.

Claim 2(a); Page 255-256; 335pp; English.

conditions, varietary, antications, controlled, controlled, controlled, antichtyroid, cerebroprotective, anotectic, condition and metabolic. Polypeptides and polynucleotides of the invention are conditioned in the treatment, or as a vaccine in the prevention of, cancer, conditioned in the treatment, or as a vaccine in the prevention of, cancer, conditioned in the treatment, or as a vaccine in the prevention of, cancer, conditioned in the treatment, or as a vaccine in the prevention of, cancer, conditioned in the prevention of, cancer, confirmantion, neoplastic diseases, nervous system related disorders and confidence in the systemic autoimmune disease, hyper-immunity, conditioned in the prevention, thyroid conditioned in the system dysfunction, thyroid conditions, pastrolic diseases, sperm dysfunction, thyroid conditions, neurological diseases, stroke, angiogenesis, controlled in the spinal cord, thyroid gland, heart, convilation disorders, diseases in the spinal cord, thyroid gland, heart, convilation diseases, and alleviation of precocious puberty. The growth abnormalities, and alleviation of precocious puberty. The sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's form the convilation in records ABQ86130-ABQ86184 represent novel human cDNA's convilation in records ABQ86130-ABQ86184 represent novel human cDNA's The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, invention

Sequence 1662 B₽; 420 A; 411 Ç 479 C 352 片 0 U; 0 Other;

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                                                                                                                                                                              AlaCysGlyMetLeuHisLeuHisGluLeuGlYIleValTyrArgAspMetLysBroGlu 320
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                                                       AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGGCTGGCCGTGGAG
                                                                                    AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
                                                                                                                                                   GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGÀAGCCTGÀG
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    ATGGTGGÁCATGGGGGGGCCTGGACAACCTGATCGCCAACACCGGCCTACCTGCAGGCCCGG

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                                                                                                                                                                                                 Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AlDS, Addison's disease; anaemia; atlergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; Good pasture's syndrome; foraves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; circhosis; Cushing's syndrome; papatitis; hypothyroidism; cerebral palsy; catearact; angina pectoris; cardiovascular disease; hypetrension; vasculitis; myocarditis; obessity; congestive heart failure; isohaemic heart disease; lung tumour; gout;
WO200196547-A2.
                                                                                                                                                             Homo sapiens.
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                             /product= "Human PKIN-19 protein"
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cc mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, costeoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, Craves' disease, crheumatoid arthritts, Sjogren's syndrome, uveitis, ulcerative colitis, crheumatoid arthritts, Sjogren's syndrome, uveitis, ulcerative colitis, comportation, parasitic, fungal, viral, protozoal and helminthic infections) cc growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, cc growth and development disorders (arteriosclerosis, cataracts); cardio cc ushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio cc aneuryems, congestive heart failure, angina pectoris, myocarditis, comportion heart disease, chronic bronchitis, lung tumours); lipid cischaemic heart disease, chronic bronchitis, lung tumours); lipid cischaemic heart disease, chronic bronchitis, lung tumours); lipid compocholesterolaemia, obesity). PKLN DNA is useful for assessing toxicity chypocholesterolaemia, obesity). PKLN DNA is useful for assessing toxicity cardio chronic promother sequence is human contact compound and in gene therapy. The present sequence is human
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23-JUN-2000;
30-JUN-2000;
07-JUL-2000;
13-JUL-2000;
25-AUG-2000;
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Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of pKIN and a composition comprising PKIN antagonist is useful for treating pKIN and a composition comprising PKIN antagonist is useful for treating pKIN antagonist is useful for treating pKIN antagonist is useful for treating a disease or condition associated with overexpression of pKIN. The adisease is considered in the cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, disorder myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder myeloma, sarcoma, teratocarcinoma, Jackima, Addison's disease, (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, altergies, adult respiratory distress syndrome, authorized the proposition of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-090207/12.
P-PSDB; AAE16273.
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1, 2000US-0213467P.
1, 2000US-0216651P.
1, 2000US-0216605P.
1, 2000US-0218372P.
1, 2000US-0228056P.
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Sequence 1662 BP; 420 A; 411 2883.00 99.82% 99.82% 99.79% .61e-282 Ç 479 Indels: Mismatches: Conservative: Matches: g. 352 0 U; 0 Other; 9 므 9 뭐 δ D. Ø U

Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

PKIN-19 cDNA

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61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGCGCGC	21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgArgSerLeUx1aueurr 	1 ATGGTGGACATGGGGGCCCTGGACACCTGAILGCCAAXACCGCCGGGGCCCTGGACAACCTGAILGCCAAXAACCGCCGGACAACCTGAILGCCAAXAACCGCCGGACAACCTGAILGCCAAXAACCGCCGGACAACCTGAACCAAAAAACCGCCGGACAAAAAAAA	1 MetValAspMetGlyAlaLeuAspAsnLeu1LeALaASpLIILALaly Leculum	US-10-044-205A-2 (1-553) x AAD26466 (1-1662)

Qy 241 GluIleLeuGluLysvalSerSerproPhelieValSerLeuHalY, Friedlick (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)
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241 GluIleLeuGluLysValSerSerProbhelleValSerLeuALdlyAntallor (11)
241 GluIleLeuGluLysValSerSerProbhelleValSerLeuhldlyAldrichen
241 GluIleLeuGluLysValSerSerProbhelleValSerLeuhld YALLEL (1)
241 GluIleLeuGluLysValSerSerProbhelleValSerLeuAldlyAldrucker
241 GluIleLeuGluLysValSerSerProbheIleValSerLeunlatyAntachculiud
221 IysleuAsplyslysArgleuLyslyslyslyslyslyslyslyslyslyslyslyslysly
1 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyUySwellYthiaVysLy (1988)
181 PheGluMetGlnProValSerAspLySTyrPhe:IIITGluFrient 9 (1987) 17 1 1 1 1 1 1 1 1 1
ASPPHOVALINESERALEERE ASPP
41 GluGIDATGVELALGALGVGITALGUTTTTTTGCAA
AACCCGCAACCCTTCCTCAGCCAGGCCGCGGCCGAGTGCCAAGTGCCAGCAGCAGCACCA
21 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 1
LJ F
81 ArgLysAlaAlaThrPheLeug-LASP also also also also also also also also
1 GAGCAGCAGCCCATCGGTCGCCGCCGCCTTCCGTCGCTAGCCTAGCCACAGTGCCCACGTT 1 GAGCAGCAGCCCCATCGGTCGCCGCCGCTTCCTTCCGTCACCTTCCTT
1 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 8
41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnbheHisSerLeuCys ou

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Identifying compounds that alter inhibition of cone opsin kinase polypeptide activity for treating a conditions related to cone visual
                                                                                 WPI; 2002-723307/78.
P-PSDB; AAE28952.
                                                                                                                                                                                                           07-MAR-2001; 2001US-0274006P.
                                                                                                                                                                                                                                                   07-MAR-2002; 2002WO-US007025.
                                                                                                                                            Bird TA,
                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7; GRK7; cone visual signalling; visual sensitivity; visual resolution; night blindness; colour blindness; Oguchi disease; Pineal gland activity; chronobiological desynchrony; depression; anxiety; memory loss; headache; mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
                                                                                                                                                                                                                                                                                                                                      WO200272541-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; antidepressant; analgesic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                           /product= "Human GRK7 protein"
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PT signaling, comprises mixing a compound with a cone opsin kinase and with XX XX Example 4; Page 45-46; 61pp; English.
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CC The present invention relates to novel human cone opsin kinase (G-protein CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides. CC The invention further relates to a method of identifying compounds that CC alter the inhibition of GRK7 polypeptide activity which involves mixing a CC determining if the test compound alters the inhibition of GRK7 protein and an inhibition of GRK7 protein activity by the inhibitory polypeptide. GRK7 sequences are useful for CC treating conditions related to come visual signalling (e.g., night CC blindness, colour blindness, difficulty with colour vision, visual contensity, Oguchi disease or dominant congenital stationary night CC intensity, Oguchi disease or dominant congenital stationary night CC depression, anxiety, mental fogginess, memory loss, headaches, fatigue, CC or jet lagi, Agonists of GRK7 polypeptide activity may be used to treat CC probes to screen for inherited disease for which increased GRK7 polypeptide CC proteceptor-mediated diseases. The GRK7 proteins are also useful in the CC come photoreceptor visual signalling or circadian rhythm, as molecular cCC and vision resolution. They are also used as gene therapy tools for individuals with such disorders. The present sequence is human GRK7 cDNA

Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Pred. No.:

Score:
Score:
Score:
Score:
Score:
Severy Matches:
Best Local Similarity:
99.82%
Query Match:
DB:

Conservative:
99.82%
Mismatches:
DB:
Gaps:
Gaps:

US-10-044-205A-2 (1-553) x AAD46350 (1-1662)

161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180 421 141 121 AsnDroGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120 301 ÁCCAAAGACAGCGCGCTGCAGGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360 241 181 121 81 61 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60 61 21 GAAGAGCGAGTGGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG AACCCGCAÁCCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420 cecanogedecia con receina con conservado de consecuencia de co ArgiysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80 GGCTGCAGGGGGGGGGGGGGGCCAGGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180 ATGGTGGACATGGGGGGCCTGGACAACCTGATCGCCAACACCGGCCTACCTGCAGGCCCGG 60 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 40

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41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLyBLeuSeLeuGuschie (1)	86	21 LysProSerAspCysAspSerLysG1uLeuG1nArgArgArgArgAseLucundur	1 MetValAspMetGlyAlaLeuAspAshLeuLLeAdAsuLL	10-044-2051		Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; V OLUCE.	The invention relates to a novel disease associated gene and the gene and its encoded protein are useful for diagnosis of and the gene and its encoded protein are useful for diagnosis of and screening for drugs for heart diseases, cancers and omentopathy. The current sequence represents a human gene sequence relative to the invention	Example 3; Page 85-86; 96pp; Japanese.	Novel disease-associated gene of the applicable in diagnosis of and scree cancers and omentopathy.	WPI; 2003-157045/15. P-PSDB; ABP60079.	Koyama N, Tanida S, Yamamoto K;	(TAKE) TAKEDA CHEM IND LTD.	15-JUN-2001; 2001JP-00182654.	14-JUN-2002; 2002WO-JP005942.	27-DEC-2002.	WO2002103020-A1.	Key Location/Qualifiers CDS 261687 /*tag= a	Homo sapiens.	Human; heart disease; cancer; omentopathy; gene; us.	Human gene sequence relative to the invention # SEQ 10	04-APR-2003 (first entry)	ABZ56943;	Л 6 5943 ABZ56943 standard; DNA; 1761 BP.			1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1820

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1226 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA
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                                             GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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                 RESULT 7
ADC39221
07-MAY-2001; 2001US-0289087P.
09-MAY-2001; 2001US-0289018P.
09-MAY-2001; 2001US-0289918P.
11-MAY-2001; 2001US-0299194P.
14-MAY-2001; 2001US-0290194P.
15-MAY-2001; 2001US-0291181P.
16-MAY-2001; 2001US-0291243P.
18-MAY-2001; 2001US-0292001P.
21-MAY-2001; 2001US-029201P.
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                                                                                                                                                                                                      02-MAY-2001; 2001US-0288063P
                                                                                                                                                                                                                                                  02-MAY-2002; 2002WO-US014199
                                                                                                                                                                                                                                                                                                   06-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; wasting disorder; Alzhelmer's disorder; cachexia; cardiomyopathy; AIDS; asthma; hemophilia; graft-versus-host disease; prostate cancer; althright scherosis; hypertension; atherosclerosis; hipertension; atherosclerosis; althright hampetension; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Albright hereditary osteodystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antilipemic; nootropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive; antiarteriosclerotic; hemostatic; osteopathic; gene therapy.; NOVX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgLeuGluAlaGlyLeuTleGluProProPheValProAspProSerValValTyrAla 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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341 986 321 301 866 281 806 261 746 241 989 221

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The invention relates to new isolated NOVX polypeptides, the genes of encoding them or sequences having at least 5% identity to the amino acid cor nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, or associated with a human disease, which includes a pathology associated with NOVX polypeptide. The NOVX polypeptide is particularly useful for cwith NOVX polypeptide. The NOVX polypeptide is particularly useful for conjupeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and complypeptide in a respecially useful for treating or preventing e.g. polypeptide are especially useful for treating or preventing e.g. conjupention, disorder, and the nove and the nucleic acid and conjupential are especially useful for treating cancer or prostate conjupential and the protein is useful in general disorders, Alzheimer's disease, conjupential assay system for conditions. The protein is useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic functional analysis of various human disorders, as well as in diagnostic infunctions. This sequence represents one of the NOVX genes of the
                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                           Alignment Scores:
                                                                  US-10-044-205A-2 (1-553) x ADC39221 (1-1821)
                                                                                                    Query Match:
DB:
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                                                                                                                                                                                            Pred. No.:
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30-MAY-2001;
31-MAY-2001;
12-JUL-2001;
31-JUL-2001;
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23-MAY-2001;
25-MAY-2001;
29-MAY-2001;
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17-AUG-2001;
10-SEP-2001;
27-SEP-2001;
27-SEP-2001;
18-OCT-2001;
28-NOV-2001;
03-DEC-2001;
03-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller CE, Kekuda R, Malyankar UM, Li L, Pena CEA, Spytek KA; Gorman L, Guo X, Fernandes ER, Smithson G, Stone DJ, Zerhusen BD; Patturajan M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR; Padigaru M, Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, Zhong M; Edinger SR, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with a human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
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P-PSDB; ADC39222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 165; 748pp; English.
                                                                                                                                                                                                                                              Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    invention.
2001US-0293107P.
2001US-0293747P.
2001US-0294109P.
2001US-0294110P.
2001US-0294434P.
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2001US-0318463P.
2001US-0325683P.
2001US-0330292P.
2001US-033873P.
2001US-033752P.
2001US-033752P.
2002US-0359245P.
2002US-00136826.
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2001US-0304879P.
2001US-0308901P.
2001US-0312270P.
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2883.00
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99.82%
99.79%
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53 ATCCTAATGGAAAAGGTAAGTTAITCLTAICCTATCTATCTATCTATCTATCTATCTATCTATCTAT	Дb
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93 ATGAAGGGTGGCAAGGCCATCACCCAGAGGGCTGGAACCAALGGLIAGATGAAGAGGGCTGGAAGGGGCTGGAAGGGGCTGGAAGGGGCTGGAAGGGGCTGGAAGGGGGTGGAAGGGGGTGGAAGGGGGGGG	ДĎ
<u> </u>	γQ
33 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCIGACCLGGGCGAGTIATGAGT 136	ф
1 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuaryacurggCCGTGGAG 10	Q
73 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGATCG	Db
on AlacysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLySerIOu-10 on AlacysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLySerIOu-10 on AlacysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMctZeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGluLeuGlyIleValTyrArgAspMctZeaHisGluCTeaHisGl	Qy
13 TACAACGTGGGCACGCGTGGACATGAGCCGGGGTGATCTTTTACTCGGCCCAGAAA	व्य
81 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 30	&)
	3 8
93 GAAAILII WAXWAXAA WAXAA WAX	₽
41 GluIleLeuGluLysValSerSerProPhellevaLaerLacord (1)	29
33 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGATGGCGAAGAAGATGGCTCTCTTGGAAAA	B &
οι IvsleuAspLysLysArgLeuLysLysLy	? !
AGATGTATGCCTGTAAG 73	욹 성
13 TTUGAGATGCAACGTTTTTTTTTTTTTTTTTTTTTTTTTT	рb
81 PheGlumetGlnProValSerAspLysTyrPheinraturnensy (1981) 1981 1982	Q
53 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGIVENGAVVACVC	рь
ProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLySLeu 10	Qγ
93 GAAGAGCGAGTGGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG	Db ;
41 GluGluArgValAlaAlaValThrLeuArgLYsAlaGluAlaMetAlaPheLeuGlnGlu 16	Q !
	D ;
21 AsnproGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 14	& £
4	\$ 8
13 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAAACTGCAGAAACTGCAGAAAGGCGGCAACCTTCCTAGAGAGAG	Db
ArgLysAlaAlaThrPheLeuGluAssPvalGlnAsnTrpGluLeuAlaGuus-us-19-19-19-19-19-19-19-19-19-19-19-19-19-	8
3 GAGCAGCCGATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCACAGTGCCCACGAGTCGCCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCACAGTGCCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTAGCAGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCCACGAGTGCACGAGTGCCACGAGTGCCACGAGTGCACGAGTGCCACGAGTGCACACGAGTGCACAGAGTACACGAGTGCACAGAGTGCACAGAGTGCACACGAGTACACACAC	рb
i Glu	QV (
41 GJYLBUGINGLYVYSALBULUEUALSJALLIJIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	} &
3 AAGCCCTCGGACTGCGACAGLAAAAGAGCTGCTGCTGCTGCTGCASnPheHisSerLeuCy	ф
21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40 	Q

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RESULT 8
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                                   New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological
                                                                                                       WPI; 2001-570872/64
                                                                                                                                     Walke DW,
                                                                                                                                                                                                                08-MAR-2001; 2001WO-US007500
                                                                                                                                                                                     10-MAR-2000; 2000US-0188449P
                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor kinase; GRK; human; ss; gene therapy; drug screening; gene expression characterisation; NHP; novel human protein.
                                                                                                                                                           (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                20-SEP-2001
                                                                                                                                                                                                                                                                          WO200168869-A2
                                                                                                                                                                                                                                                                                                                                                                          Human G-protein coupled receptor kinase 3 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                           Wilganowski NL, Turner CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1692
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밁 Ś 망 Ś 밁 Ş DЪ Ş

> CC The present CDNA sequence encodes a human G-protein coupled receptor CC kinase (GRX), also designated MHP (novel human protein) in the specification, which is shown in the sequence listing. The invention CC similarity to G-protein coupled receptor kinases. Oligonucleotides CC derived from the nucleotide and protein sequences which have CC grobes for screening libraries and assessing gene expression patterns. CC probes for screening libraries and assessing gene expression patterns. CC gene therapy for the modulation of GRX expression. The nucleotides of the invention are also useful in drug screening and CC invention can be used to genetically engineer host cells to express GRX CC useful in addressable arrays for identifying and characterising the CC temporal and tissue specific expression of a gene and in microarrays to CC screen collections of genetic material from patients who have a local condition. The proteins of the invention are also cc in assays for screening for compounds that are useful in the treatment of comental, biological or medical disorders/diseases

Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

Query Match:

Best Local Similarity:

2883.00 99.82% 99.82% 99.79% 1.16e-281

Conservative: Mismatches: Indels:

0010

Matches: Length:

Gaps:

Percent Similarity:

Pred. No.: Alignment Scores:

밁 Ş B 8 밁 á 밁 Ś 뮍 Ś 뮍 Ś 밁 Ś 뮍 Ś 밁 á B Ś US-10-044-205A-2 (1-553) x AAH78799 (1-2249) 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220 181 161 141 774 714 121 654 ACCAAAGACAGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 101 ThTLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 594 534 GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 474 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyBro 100 354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 13 41 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaWetAlaPheLeuGlnGlu 160 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 953 CAGCCCTTTAAGGÁTTTCGTGÁCCAGCGCCTTCTÁCGÁCAAGTTTCTGCÁGTGGÁÁÁCTC 893 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACCAAGTGCCAAGCAGCCACCACTGAG AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGGAGCTGGCCGAGGAGGGACCCC GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80 GGGCTGCÁGGGCTGCGCGAGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60 833 713 120 653 593 533 473 413 20

Disclosure; Page 33-34; 34pp; English

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ACC44827 standard; cDNA; 3186

04-JUN-2003 (first entry)

Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.

neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant; vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder; central nervous system disorder; cardiovascular disorder; asthmat CODP; chronic obstructive pulmonary disorder; antiety; mood disorder; enzyme; Alzheimer's disease; Parkinson's disease; congestive heart failure; myocardial infarction; ischaemic disease; hypertensive vascular disease; gene; Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;

Homo sapiens.

CDS 85. .1746 /product= "G protein-coupled receptor kinase (GRK)" /*tag= location/Qualifiers

WO2003018815-A2.

06-MAR-2003

19-AUG-2002; 2002WO-EP009235

21-AUG-2001; 2001US-0313464P

(FARB) BAYER AG

Xiao ĸ

WPI; 2003-278669/27. P-PSDB; ABP96709.

New G-protein coupled receptor kinase polypeptides and polynucleotides, useful in identifying modulators of the enzyme for treating cancer, diabetes, a central nervous system disorder, a cardiovascular disorder or

Claim 1; Fig 11; 129pp; English.

The present sequence encodes a human G protein-coupled receptor kinase CC (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective, CC (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective, CC (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective, candiovascular, anti-Parkinsonia, cardiant, vasotropic and CC antiasthmatic activities, and can be used in gene therapy. (I) can be CC regulated to treat cancer, diabetes, a central nervous system (CNS) CC regulated (e.g. anxiety or mood disorders, Albheimer's disease and CC Parkinson's disease), cardiovascular disorders (e.g. congestive heart or CC failure, myocardial infarction, ischaemic diseases of the heart or hypertensive vascular disease), asthma and chronic obstructive pulmonary CC disorder (COpD). GRK molecules are useful in screening for agents that CC regulate or decease the activity of a GRK. GRK sequences may also be used CC and abnormalities or susceptibility to diseases CC and abnormalities or susceptibility to diseases CC and abnormalities related to the presence of mutations in the nucleic CC and sequences that encode the GRK enzyme

Sequence 3186 BP; 857 A; 737 C; 784 G; 808 Η. 0 U; 0 Other;

US-10-044-205A-2 (1-553) x ACC44827 (1-3186) Query Match: Best Local Percent Similarity: Score: Alignment Scores: NO:: Similarity: 1.89e-281 2883.00 99.82% 99.82% 99.82% 99.79% Length: Matches: Gaps: Mismatches: Conservative: Indels:

RESULT 9 ACC44827

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1045 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1104
              361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
                                                                                           341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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                                                              ATGAAGGGTGGCAAGGCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164
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WPI; 2002-130533/17.
                                      Guegler K, Di Francesco V,
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18-DEC-2000; 2000US-00738894
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                                                                                           (APPL-) APPLERA CORP
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                                                                                                                                                                                                                                                                                                                                  /product= "Human kinase protein"
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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P-PSDB; AAE17136.

New isolated human kinase proteins and nucleic acids, useful as a major target for drug action and development, particularly for screening modulators of the kinase peptides.

Claim 4; Fig 1; 87pp; English.

AX The invention relates to human kinase proteins that are related to Grotein coupled receptor kinase subfamily. Human kinase gene is located CC protein coupled receptor kinase subfamily. Human kinase gene is located CC on chromosome 3. The kinase peptide and nucleic acid are useful in the corresponding protein subsetul as a major target for drug action and development, and is compositions. The peptide CC valuable to the field of pharmaceutical development to identify and CC valuable to the field of pharmaceutical development to identify and CC raise antibodies or to elicit an immune response, as a reagent in assays crase antibodies or to elicit an immune response, as a reagent in assays fluids and as markers for tissues in which the corresponding protein is CC fluids and as markers for tissues in which the corresponding protein stage of tissue differentiation or development or in a disease state). The CC of tissue differentiation or development or in a disease state). The CC disease or predisposition to disease mediated by the peptide. The nucleic CC disease or predisposition to disease mediated by the peptide. The nucleic acid molecules are useful for probes, primers, chemical intermediates and CC acid molecules are regulatory regions of the nucleic acid molecules and CC containing the gene regulatory regions of the nucleic acid molecules and CC for drug screening to identify compounds that modulate kinase nucleic for drug screening to identify compounds that modulate kinase nucleic acid expression. The present sequence is human kinase cDNA expressed in CC skins, germinal center B cells, colon, kidney and lung

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Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;

044-205A-2 (1-553) 1 MetValAspw	Alignment Scores: Pred. No.: Score: Percent Similarity Percent Local Similar Query Match: DB:
	ment Scores: No.: standarity: nt Similarity: Local Similarity: Match:
) x AADZ8071	
(1-1662) SpashLeuIleAlaAs	Length: Matches: Conservative: Mismatches: Indels: Gaps:
MetValAspMetGlyAlaLeuAspAsmLeuIleAlaAsmThrAlaTyrLeuGlnAlaArg 20	1662 551 0 2 0

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01 GATAAGCAGTTCTTCAAAAACTTTTGCGACAGGTGCIGIIGIIGIIGIIGIIGIIGIIGIIGIIGIIGIIGIIG	Дb
1 AsplysGlnphePheLysAsnPheAlaThrGlyAlaValPrOlleA.ataPysLysChild	8
41 AAAGACATOGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGGTGGAATTTGATGACA	망
81 LysaspilealaGluIleaspaspPheSerGluValArgGlyValGluPheAspAspLys 50	Q ;
 TATGCC 14	B &
21 AGCAGAGAAAAGTCTGATGATGCLAGGAGAACATCCTTTTTTTTTT	ממ
41 SerArgGluTysSerAspAspProArgTysHisHisPhePheTysIIII1eAsuriccii	γQ
	망
21 GluGjuAlaTysAspIleCysArgLeuPheLeuAlaTysTysProGluGlnArgLeuGly 44	Q 5
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TTTATGAAATGGTTGCTGGACGAACGACCATTCAAAGALLACAANSSTAATSUU	망
81 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLySULLLySvalseLyS	Qy
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361 IleLeuMetGluiysVal8erTyrSerTyrProValAspTrpPheAlaMetGlyCySSer 300	Ş
ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTCGGAACCAATGGTTACATGGCTCCTGAG 10	당
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GCCTGTGGGAIGCIGCACCICCICCICGTGGAAIGCIGCACCACGACGAAGCACACGACGACGACGACGACGACGAC	В
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CTGCAGTGGAAACTC 54	물 왕
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XX Poly
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                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                 Query Match:
                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                      disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides emodding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polyneptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS06701-AAS06757 encode for novel human protein kinases #1-57. The nove serine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), metabolic disorders (e.g. diabetes), and the polypeptides may be used to treat disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), metabolic
                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                 Sequence 1662
                                                                                                                                                                                                                                                                                              protein kinase expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 433pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUGE-) SUGEN INC.
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Human, G protein coupled receptor kinase; GRK; cytostatic; antidiabetic; neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant; vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder; central nervous system disorder; cardiovascular disorder; asthma; COPD; chronic obstructive pulmonary disorder; anxiety, mood disorder; enzyme; chronic obstructive pulmonary disorder; anxiety, mood disorder; enzyme; Alzheimer's disease; Parkinson's disease; congestive heart failure; Alzheimer's disease; parkinson's disease; hypertensive vascular disease; myocardial infarction; ischaemic disease; hypertensive vascular disease;
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                                        Xiao Y;
                                           (FARB ) BAYER AG
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WPI; 2003-278669/27.

New G-protein coupled receptor kinase polypeptides and polynucleotides, useful in identifying modulators of the enzyme for treating cancer, diabetes, a central nervous system disorder, a cardiovascular disorder (diabetes). P-PSDB; ABP96707

Claim 1; Fig 1; 129pp; English.

sequences that encode the GRK enzyme

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                               /product= "Human GRK7 OK6 splice variant protein"
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07-MAR-2002; 2002WO-US007025.

19-SEP-2002.

07-MAR-2001; 2001US-0274006P

IMMUNEX CORP

Bird TA, Spencer M, Mosley

WPI; 2002-723307/78. AAE28953.

Identifying compounds that alter inhibition of cone opsin kinase polypeptide activity for treating a conditions related to cone visual signaling, comprises mixing a compound with a cone opsin kinase and with an inhibitory polypeptide.

Example 4; Page 48-49; 61pp; English.

CC The present invention relates to novel human cone opsin kinase (G-protein CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides. CC alter the inhibition of GRK7 polypeptide activity which involves mixing a CC elect compound with GRK7 protein and an inhibition of GRK7 protein and an inhibition of GRK7 protein and continuous activity by the inhibitory polypeptide. GRK7 sequences are useful for CC detaining conditions related to cone visual signalling (e.g., night CC blindness, colour blindness, difficulty with colour vision, visual sensitivity, visual resolution or in adapting to changes in light CC intensity, Oguchi disease or dominant congenital stationary night CC depression, anxiety, mental fogginess, menory loss, headaches, fatigue, CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat CC activity is beneficial, e.g., decreased colour sensitivity or other cone CC photoreceptor-mediated diseases. The GRK7 proteins are also useful in the

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Best Local Similarity:
Query Match:
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ABZ56934; ABZ56934 standard; DNA; Human; RGSNo9; heart 04-APR-2003 (first entry) ВP

Human RGSNo9 encoding DNA # SEQ ID 2.

disease; cancer; omentopathy; gene; gs

Homo sapiens

Location/Qualifiers

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Koyama N,

ABP60078

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US-10-044-205A-2 (1-553) x ABZ56934 (1-1191)
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                                                                                                                                                                                                                                                                                                                                        G-protein coupled receptor kinase; GRX; human; ss, drug screening; gene expression characterisation; novel human protein.
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Percent Similarity: Best Local Similarity:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NHP (novel human protein) in the specification, which is claimed in the invention. The invention comprises specification, which is claimed in the invention. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides derived from the nucleotides of the invention are useful as hybridisation probes for nucleotides of the invention are useful as hybridisation probes.
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Oy 321 ASDVALLEULEUASPASPLEUGIYASDCSTATGLEUSETASPLEUGIYASDCSTAGAS (1988)
Db 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG
41
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgVallIlePheTyrSerAlasInLte Qy 1
Db 781 AAGACCCATCTCTGCCTTGTCATGAGCCT
Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisTle Qy 1
Db 721 GAAATCTTGGAGAAGGTCAGCAGCCCTTT
Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer
Db 661 AAACTGGACAAGAAGCGCTGAAGAAGAA
Qy 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyGluLysMetAlaLeuLeuGluLys
Db 601 GGTTTTGGGGAGGTATGTGCCGTCCAGTC
201
Db 541 TTCGAGATGCAACCAGTGTCAGACAAGTAC
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGLY
Db 481 CAGCCCTTTAAGGATTTCGTGACCAGCGCC
Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu Qy 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu
pb 421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCC
Qy 141 GluGluArgValAlaAlaAlaValThrLeuArgLygAlaGluAlaMetAlaPheLeuGlnGlu Qy
361 AACCCGCAACCCTTCCTCAGCCAGGCCGTG
121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu
301 ACCAMAGACAGCGCCTGCAGGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG

Search completed: August 13, 2004, 19:14:24 Job time : 481 secs

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-MODEL-ETREME+ PAR. model -DEV=xlh
-MODEL-ETREME+ p2n. model -DEV=xlh
-Q=/Cgn2_1/USFTO_spool/US10044205/runat_06082004_104322_23369/app_query.fasta_1.711
-DE-EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UTTEME-200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=US10044205_@CGN 1_1_2607_@runat_06082004_104322_23369 -NOPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

Homo sapiens

BC027597.1 GI:20379554 Homo sapiens (human)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2329)

RESULT 1
BC027597
LOCUS
DEFINITION

BC027597

EC027597 2329 bp mRNA linear HTC 01-MAY-200 Homo sapiens, Similar to G protein-coupled receptor kinase 2-like (Drosophila), clone IMAGE:4830673, mRNA.

HTC 01-MAY-2002

ALIGNMENTS

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

38 40 41 42 43		25 26 27 28 29 30	17 C 18 C 19 C 20 C 21 C 22 C 23 C 24	0 155 150 150 150 150 150 150 150 150 15	Result No. 1.2.2.3 3 3 3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
700 697.5 696.5 692.5 690.5 685	728.5 720.5 717.5 712.5 702.5 700.5	737.5 737.5 737 731.5 731.5 731.5 729	780 767.5 762.5 761.5 761.5 761.7 752 747.5 747.5 737.5	826.5 813.5 803.5 796.5 793 793 793 793 793	Score 1262 1219.5 1218.5 955.5 940.5 883.5
24.2 24.2 24.1 24.1 24.1 23.9 23.9 23.7 23.6	25.2 24.9 24.8 24.7 24.7 24.3	2 2 2 2 2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5	26.6 26.4 26.3 25.9	28.6 28.5 27.8 27.6 27.4 27.4 27.2	991277144
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US-10-044-205A-2 QY 7 Lei	Alignment Pred. No.: Score: Score: Percent Si Best Local Query Matc DB:	FEATURES SOUICE ORIGIN	REMARK COMMENT	AUTHORS TITLE JOURNAL
7 LeuAspAsnieuIleAlaAsnThrAlaTyrieuGlnAlaArgLysProSerAspCys 25	Scores: 7.86e-117 : 1262.00 imilarity: 65.43% I Similarity: 47.40% ch: 43.68%	Clone c through Series clinis clipassed This clinhis cl	-MGC Project URL: http://mgc.nci.nih.gov tract: MGC help desk il: cgapbs-remail.nih.gov il: cgapbs-remail.nih.gov isue Procurement: Miklos Palkovits, M.D., Ph.D. isue Procurement: Miklos Palkovits, M.D., Ph.D. iniyaki and Piero Carninci (RIKEN) hiyaki and Piero Carninci (RIKEN) iniyaki and Piero	Strausberg,R. Direct Submission Direct Submission Submitted (08-APR-2002) National Institutes of Health, Mammalian Submitted (08-APR-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                          Akhter, N., Ayele, K., Beekstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.I., Granite, S., Guan, X., Gupta, J., Haphighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. C., McDowell, J. Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 AlaTrpGln---Glu-GluIleIleGluThrGlyLeubheGluGluLeuAsn 531
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                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                            Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consortium (LLNL)
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US-10-044-205A-2 (1-553) x BC057206 (1-2989)
199 LysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAla
                                                            687 AAGTGGCTGGAAAGGCAACCAGTGACCAAAAACACCTTCAGGCAGTACCGAGTCCTGGGC
                                                                                                                                                                                                                                                                                                139 ThrGluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
                                                                                                                                                                                                                                                                                                                                                  534 CGGCAGCTGGTGAGTAACTGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAGACCTCTTC 593
                                                                                                                                                                                                   159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp 178
                                                                                                                                                                                                                                                               594 CAGGAGCTGACCCGGCTG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: m Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7242151
This clone has the following problem: frame shifted.
                                                                                                                                                        AGCACGGCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTTCTGCAGTGG
                                                                                                 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                 GlnProPheLeuSerGlnAlaValAlaThr-----LysCysGlnAlaAlaThr 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCTGGATGGGGTĞTCTGAATATĞAĞGTGACCCCTGATGAGAAGCGGAAAGCATGTGGG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAspSerAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCGCCTGTTATTTCGTGAGTTCTGTGCTACGAGACCTGAGCTGACCCGGTGTACTGCC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGACTAATGCAGAACTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGAAGTTCCA
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/lab_host="DH10B"
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                                               enriched library, clc
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                              Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-resegsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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6 (bases 1 to 2978)
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Analysis of the mouse transcriptome based on functional
of 60,770 full-length cDNAs
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                      URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
                                                                      prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                         Division of Experimental Animal Research in Riken
                                                                                                                                          Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome
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Qy 190 rPheThrGluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnVa 210	OY 131 ALATHRIPSCYSGLARIAALATHRTHNGIUGIUGIUATGVAIALAALA-VAITHRIEUAR 150 150 SIYSALAGUALAMEALAHALAGUANGACCTCTTCCAGGAGCTGACCGGCTG	370 94 430 111 1490	250 54 310 74	ignment Scored. No.: ore: recent Similar recent Similar st Local Sin ery Match: :	/clone="D130046K22" /tissue_type="spinal ganglion" /clone Tib="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" misc_feature 2561993 /note="G_PROTEIN-COUPLED_RECEPTOR_KINASE_GRK6 (EC 2.7.1) homolog [Mus musculus] (SWISSPROT 070293, evidence: FASTY, 100%ID, 96.9%length, match=1714) ORIGIN	FEATURES Location/Qualifiers 12978 /organism="Mus musculus" /mol_type="mgNA" /strain="C57BL/65" /db_xref="FATYOM_DB:D130046K22" /db_xref="taxon:10000"
RESULT 4 AY406080 LOCUS LOCUS AY406080 DEFINITION Homo sapiens GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION VERSION AY406080 VERSION AY406080.1 GSS. SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	489 eSerGilvalArgGilvalGuPheAspAspLysGlnPhePheLysAsnPheAl 509	1429 TCTTA 449 9LysH :::: 1489 GGAGC 469 OPROP 1549 ACCTT	1312 CTTCC 410 pGluV : 1369 AGTGG	1135 350 1195 370 1252	Oy 290 tSerArgValllePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisGluLe 310	Qy 250 ellevalSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLe 270

Qy 124 ProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGluGluArg ::: pb 318 GACCTGGTCTCCCAGACGAGGAGAAGCTCCTACAGAAGCCGTGCAAAGAACTCTTTTCT 377 QY 144 ValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGluGlnProPhe 163 QY 154 ValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGluGlnProPhe 163 QY 164 LysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeuPheGluMet 183 QY 164 LysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeuPheGluMet 183 QY 184 GlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGlyGPheGly 482 QY 184 GlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGlyGPheGly 203 QY 483 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1-2 (1-553) x AY406080 (1-1721) LeuAlaLeuProGlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPhe	COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers 1. 1721 Location/Qualifiers 1. 1721 /mol_type="genomic DNA" /db xref="teaxon:9806" gene /1. 172. /gene="gPRK5" /locus_tag="HCM2438" ORIGIN Alignment Scores: Pred. No.: 955.50 Percent Similarity: 41.95% Best Local Similarity: 41.95% Best Local Similarity: 41.95% Best Local Similarity: 41.95% Best Local Similarity: 43.07% Best Local Similarity: 43.07	AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenhaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE gene trios JOURNAL promise or thologous prometric clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., PEFERENCE 2 (bases 1 to 1721) REFERENCE 2 (bases 1 to 1721) Formitte Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Fodd, M.A., Tanenhaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE phret Submission Total Communication of the communic
AY406082 DEFINITION Mus musculus GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION AY406082 VERSION AY406082.1 GI:39762056 KEYMORDS SOURCE Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus. REFERENCE 1 (bases 1 to 1721) 1 (bases 1 to 1721) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	YELYSGINLYSVAISERLYN		204 543 224 603 244 663 264

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                                                                                          190 TyrPheThrGluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGln 209
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/mol_type="genomic DNA"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                   Contact: Genoscope
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3090.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAAO4AGO3NP1&cluster=3090.f. Contact:
Reng Iiang Email: fliang@lifetech.com URL:
Reng Iiang Email: fliang@lifetech.com URL:
Reng Avenue Genoscope sequence ID: CSOAAO04AGO3NP1.
Faraday Avenue Genoscope sequence ID: CSOAAO04AGO3NP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 MetAlaLeuLeuGluLysGluIleLeuGluLysVal8erSerPropheIleValSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLys 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ÁTGGCGCTGAACGÁGAÁGCAGATCCTGGÁGAAAÁGTGAACÁGTAGGTTTGTAGTGÁGCTTG</u>
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                                                                                                                                                                                                                                                                                                                                     PheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyr 314
                                                                                                                                                                                                                                                                                                                                                                                     AspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgVallle 294
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                                                                                                                                                                                             AGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGAC 524
                                                                                                                                                                                                                                        ArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAsp 334
GlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrp 374
                                                                                               CTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTG 464
                                                                                                                                          LeuGlyLeuAlaValGluMetLysGlyGlyLysProileThrGlnArgAlaGlyThrAsn 354
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institutes of Health, Mammalian
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/gcacGaG(G). Size-selected >510mp for average insert size
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/labb Library constructed by Ling Hong in the laboratory
/of Gerald M. Rubin (University of California, Berkeley)
/of Gerald M. Rubin (University of California, Berkeley)
/of Gerald M. Rubin (Stratagene) and Superscript
/lab Library CDNA synthesis kit (Stratagene)
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Best Local Similarity: Percent Similarity: Alignment Scores:

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Score:

Pred. No.:

EST 29-MAR-2002 IMAGE:5813275

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US-10-044-205A-2 (1-553) x BQ066445 (1-968)
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                                                                          529 GluLeuAsnAspProAsnArgProThrGly 538
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                                       GAACTTAAT-----GGTACCCCTTCCGGC 920
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                                                                                                     ATCCCATGGCAAAACCAGATGATAGAAACCGAATGCTTTAAAGGACCTGAACCTGGTTTG 896
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TÄTGCGĠĊĀGAGĀŤĊCTCTĠĊĠĠĊTTAGAAGACĊŤĊĠĀĊCGTGAGAACACCĠŤĊŤĀĊĊĠĀ
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 998)
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AGENCOURT 7047352 NIH MGC 99 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; CNNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                    1017 bp mRNA linear EST 02-APR-200;
AGENCOURT 6862973 NIH MGC 99 Homo sapiens cDNA clone IMAGE:5920182
5', mRNA sequence.
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                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                       Unpublished
                                                                                                                                                   National Institutes of Health, Mammalian Gene
                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                      363 TACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCCGACTACTGG 419
                                                                                                                                                                                                            376
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                       436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisHisPhePhe 454
                                                        540
                                                                              416 HisaspasnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPro 435
                                                                                                                    480
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                                                                                                                                                                               420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGAC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyralapheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAsp 275
                                                                                                                                                                                                                                                                                                                             GlyLeuAlaValGluMetLysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGly 355
                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrSeralaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGAGGCCTTGTTT 182
                                                                                                                                                                                                                                                                                                  ĠĠĊŦŦĠĠĊŦĠŦĠAAGAŦĊĊĊĠAĠĠĠĀĠĀĊĊŦĠĀŤĊĊĠĊĠĠĊĊĠĠŦſĠĠĠĊĀĊŦĠŦŦĠĠĊ
                                                                                                                                                                                                                                                                                                                                                            GATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTG 302
                                                                                                                                                                                                                                                                                                                                                                                       AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArqLeuSerAspLeu 335
                                                                                                                                                                                                                                                                                                                                                                                                                      TATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGA
                                                                                                                  ĠĀĠĀĀĠĠŦĠĀĀĠCŒĠĠĀĠĠĀĠĠŦĠĠĀĊĊĠĠĠŦĊĊŦĠĠĀĠĀĊĠĠĀĠĠĀĠĠŦĠŦĀĊŦĊC 539
                                                                                                                                             GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
                                                                                                                                                                            AlaMetGlyCyeSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
                                                                                                                                                                                                                                                            TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhe 375
                                                      cac---aagtitetecgággággéchagtechitetgeaagatgetgétéaggááagatgeg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:5920182"
/tissue_type="lymphoma, cell line"
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813.50
71.72%
51.85%
28.16%
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Indels:
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Matches:
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154
59
81
3
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62

242

362

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Query Match:
                                                  Percent Similarity:
Best Local Similarity:
                                                                                                             Pred. No.:
                                                                                                                               Alignment Scores:
                                                                                               Score:
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     777 GTCAATCTGGACCACAGACGACGACGTTCTACTCCAAGTTCTCCACGGGCTCTGTGTCC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                717 CCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGGTGAAGGC 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 AGGAACATGÁACTTCAAGCGCTTAGÁAGCCGGGATGTTGGACCCTCCCTTCGTTCCÁGÁC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 LysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAsp 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2083 row: h column: 05
High quality sequence stop: 704.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ061148 1019 bp mRNA linear EST 02-APR-2002 AGENCOURT 6862941 NIH MGC 99 Homo sapiens cDNA clone IMAGE:5920180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValPro 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 1019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGly 494
                                                                                                                                                                                   /tissue_type="lymphoma, cell line"
/lab host="DHIOB (phage-resistant)"
/clone_lib="NHIOB (phage-resistant)"
/clone_lib="NHI MGC 99"
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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                                                                                                                                                                                  Library."
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5920180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="mRNA"
             9.58e-71
803.50
72.54%
53.17%
27.81%
                                                                                                                                                                                                                                                                                                                                                                                                                          xref="taxon:9606"
                           Mismatches: Indels:
                                                                  Conservative:
       1019
151
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BQ063841
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                                                                                                                                                                                                   852 GAACGCCTGGGG 863
                                                                                                                                                                                                                                      437 GlnArgLeuGly 440
                                                                                                                                                                                                                                                                  792 AGCGCTTTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCC
                                                                                                                                                                                                                                                                                                 417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
                                                                                                                                                                                                                                                                                                                                                                           397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
                                                                                                                                                                                                                                                                                                                                                                                                                                  672
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                                                                              AGENCOURT 6832078 NIH_MGC_99 Homo FORESO ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 GlnTrpLYsLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu
                                                  BQ063841.1 GI:19891943
             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 CAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 TACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTG
                                                                                                                                                                                                                                                                                                                                          CTCGGCTGCCTCTTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTGNGA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGCTCCGGAGGTGGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysG1yG1yG1uLysMetAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAlaGlnIleAlaCysGlyMetLeuHisGeuHisGluLeuGlyIleValTyrArgAsp 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTTCCACATCTACCACATGGGCAGGCCTGGCTTCCCCGAAGCGCGGGGCCGTCTTCTAC
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                                                                                                 mRNA linear E
sapiens cDNA clone
                                                                                                                 EST 02-APR-2002
                                                                                               IMAGE:5925495
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276 314

254

194 216 134 196 74

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REFERENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               303
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Tissue Procurement: Lou Staudt
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLCM2097 row: e column: 16
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                                                                                                             GATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTG 302
                                                                                                                                 AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeu 335
                                                                                                                                                                           TATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGA 242
                                                                                                                                                                                                                                         CTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGGGGCCTTGTTT 182
                                                                                                                                                                                                                                                             LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe
                                                                                                                                                                                                                                                                                                      TATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGAC
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                                                                                                                                                                                                         TyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
          TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhe 375
                                             ĠĠĊŦŦĠĠĊŦĠŦĠAAGATCCCCGAGĠĠĀGACCTGĀŦĊCGCGGCĊĠĠĠŦĠĠĠĊĀĊŦĠŦŦĠĠĊ
                                                                         GlyLeuAlaValGluMetLysGlyGlyLysPro[leThrGlnArgAlaGlyThrAsnGly 355
quality sequence stop: 604
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/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisHisPhePhe 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU526699 934 bp mRNA linear ES' AGENCOURT 10181837 NIH MGC_101 Homo sapiens cDNA clone IMAGE:6536408 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 934)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLCM2697 row: 1 column:
                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTCATCTGGNACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGCTCTGTGTCC 836
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                                                                                                                                                                                                                quality sequence stop: 640.
/clone="IMAGE:6536408"
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                                                                                                                                                                                    Location/Qualifiers
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US-10-044-205A-2 (1-553) x BU526699 (1-934)

Query Match: DB:

Best Local Similarity: Percent Similarity:

9.92e-70 793.00 71.93% 52.98% 27.45%

Indels: Mismatches: Conservative:

934 151 54 78 2

Score:

Alignment Scores:

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397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 137
                                                                                                                                                  MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
                      AAAGTGAAGCGGGNAGGAAGTGGACCCGCCGGTTCCTGGAGACGGGAGGAGTGTACTCCC
                                                                                                                    ATGGCTCCAGAGGTCCTGAAACACCAG---AGGTACGGCCTGAGCCCCGACTACTGGGGC 734
                                                                                                                                                                                                                                                            MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
                                                                                                                                                                                                                                                                                                            TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGNCGGGTGGGCACTGTTGGCTAC 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGGGCCCTTGTTTTAT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 437
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/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2: XhOI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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http://image.llnl.gov
Plate: LLCM2064 row: j column: 03
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Location/Qualifiers
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Tissue Procurement: Lou Staudt
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_6739297 NIH_MGC_99 Homo
5', mRNA sequence.
CAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTC
                                          GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArqVal 196
                                                                                          TACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTG 74
                                                                                                                                     PheLeuGlnGluGlnPropheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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/tissue_type="lymphoma, cell line"
/lab host="PHI08 (phage-resistant)"
/clone_lib="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRIXhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size 1.8bb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMA
Homo sapiens cDNA clone CSODL010YD11 3-PRIME, mRNA sequence.
BX392018
                  Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891 CCTCATCCCTAAGTCCCCCGGCAGCTGGTGACGACCTGCACCCAGCGGCTGNAGCAGGGT 832
                                                                                                                                                                                                                                                         009
                                                                                                                                                                                                                                                                                          219
                                                                                                                                                                                                                                                                                                                              660
                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                                                     720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
BB 191 91006 ENRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This seguence belongs to sequence cluster 3090.f For
                                                                                                                                                                                   540
                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgi-bin/cluster.cgi?seq=CSOBAI046ZH12 CSO4416 1&cluster=3090.f. Contact: Feng Liang Email: fliang@llfetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSOBAI046ZH12_CSO4416_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     more information about this cluster, see
                                                                                                                                                                                                                                                                                                                            AAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCC
                                                                                                                                                                                                                                                                                                                                                  LysG1yG1yPheG1yG1uValCysAlaValG1nValLysAsnThrG1yLysMetTyrAla 218
                                                                                                                                                                                                                                                                                                                                                                                                                                 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArqValLeuGly 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGTGGCCCTTTTTGCCCACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTGCAAAGACCTTTTTCAGGAACTCACCCGGCTGACCCACGAG-----TACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proGlnproPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu--- 140
                                                                                                                                                                                                                                                       TGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAAGGCCATGGCGCTGAAC 541
                                                                                                                                                                                                                                                                                                                                                                                                   AAGTGGCTGGAAAGGCAAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGC
                                                                       HisīleTyrAsnValGlYThrArgGlYLeuAspMetSerArgValIlePheTYrSerAla
                                                                                                            GAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGGGACCTCAAGTTC
                                                                                                                                   GluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPhe
                                                                                                                                                                                 ĠĀĠĀĀĠĊĀĠĀŤĊĊŤĠĠĀĠĀĀĀĠŦĠĀĀCĀĠŤĀĢĠŤŤŤGŦĀĠŤĠĀĠĊŤŤĠĠĊĊŤĀĊĠĊĊŦĀT
                                                                                                                                                                                                        GluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPhe
                                                                                                                                                                                                                                                                                 CysLysLysLeuAspLysLysArgLeuLysLysG1yG1yG1uIysMetAlaLeuLeu 238
                                         ||||||||||::::::|||
| CACATCTACCACATGGCCAGGCTGGCTTCCCCGAAGCGCGGCCGTCTTCTACGCCGCC
| CACATCTACCACATGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLONE="CSODIO10YD11"
/cell type="B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED"
/cell line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.37e-69
791.50
72.82%
51.92%
27.40%
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Indels:
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Matches:
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917 149 60 71 7

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SOURCE
ORGANISM
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 SerLysGluAspLeuLysGln 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 ValGlumetLysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGlyTyrMetAla 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 GlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLys 318
                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: m13r, 5' TTTCACACAGGAAACAGCTATGAC 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPDLIB; I.M.A.G.E. CDNA Clone Collection (amp- resistant) (RZPDLIB NO.998) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AAGCGGGAGGAGGTGGAGCGG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +49 30 32639 101 Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
Unpublished (2003)
Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heil, O., Neubert, P., Peters, M., Rade Schroth, A., Korn, B. and Landgrebe, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EX849055
BX849055 Xenopus laevis oocyte Xenopus laevis cDNA clone IMAGp998G249027; IMAGE:3746735 5', mRNA sequence.

EX849055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RZPD; IMAGp998G249027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX849055.1 GI:39744402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (enopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TĠĊCTCCTGTÁĊĠÁĠÁTĠATCĠĊÁĠĠĊCAGTCGĊĊĊTTĊCAGCAGAGGÁÁĠAAGÁÁĠATC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGGCATCTCTGACCTGGGACTAGCT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuGerAspLeuGlyLeuAla 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 838)
                      /clone="IMAGP998G249027; IMAGE:3746735"
/tissue_type="occyte (stages 5 and 6)"
/lab host="Top-10 f''
/clone=lib="Xenopus laevis occyte"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site_2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA.
EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                       organism="Xenopus laevis"/
                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
SS-library phagemids were prepared by mass excision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Radelof, U., Schneider, D.,
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COMMENT

TITLE

VERSION

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> from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 Fr. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene Collection (XGC) library."

IleLeuMetGluLysValSe	ω	δ.
1 MetLysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu :::	y 341 b 623	유 5
1 AsnValleuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu ::: :::::: :::	Qy 32 Db 56	п о
	σ ω	н - ~
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1 LysThrH1sLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 	ωκ	
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05A-2 (1-553) x BX849055 (1-838)	US-10-044-2	
3.48e-69 Length: 838 787.00 Matches: 152 71.18* Conservative: 53 Similarity: 52.78* Mismatches: 60 27.24* Indels: 23 13 Gaps: 4	Pred. No.: Score: Score: Percent Simi Best Local S Query Match: DB:	

FEATURES

Search Job tim	DЪ	S)	ДЬ	γQ	Db
Search completed: August 13, 2004, 21:10:27 Job time : 2727 secs	800 GGGAAAGAGGTTGAAAAAAAGG 821	400 sGluAspLeuLysGluArg 406	740 ATTTATGAGATGATCGAAGGGCCATCTTCCCTTTCGGCACGGGAAAGAACGAGTAAAAAA 799	381 IleTyrGluMetVal-AlaGlyArgThrProPheLysAspTyrLysGluLysValSerLy 400	683 GTGATAAAGAATGAACGCTACACTTTTAGCCCCGGACTGGTGGGGTTTTGGGTTGTCTC 739

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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MODEL-frame+_p2n.model -DEV=x1h
-Q=/cgn2 1/USPTO_spool/US10044205/runat_06082004_104323_23382/app_query.fasta_1.711
-DB=Issued_Patents_NA _QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRATT=1 -RMD=-1 -MATRIX=blosum62 -TRANG=human40.cdi
-LIST=45 -DOCALICNS=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIEZE=500 -MINLENE=0 -MAXLEN=200000000
-USER=US10044205_GCGN_1 1.54 @FUNAt _06082004_104323_23382 -NCPU-6 -ICPU=3
-USER=US10044205_GCGN_1 1.54 @FUNAt _06082004_104323_23382 -NCPU-6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -SPBLOCK=100 -LONGLOG
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -SPBLOCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -PGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                             No.
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9
10
11
12
                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1280.5
1252.5
1252.5
1252.5
1252.5
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                                                                                                                                             1801
                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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5: /cgn2_6/ptodata/2/ina/pcTUS COMB.seq:*
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Š US-10-044-205A-2 (1-553) x US-09-802-117-1 (1-1662) Query Match: Best Local Similarity: Pred. No.: Alignment Scores: US-09-802-117-1 Percent Similarity: NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 GENERAL INFORMATION: CURRENT APPLICATION NUMBER: US/09/802,117 CURRENT FILING DATE: 2001-03-08 PRIOR APPLICATION NUMBER: US 60/188,449 PRIOR FILING DATE: 2000-03-10 APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, Nathaniel L. APPLICANT: TUTNer, C. Alexander Juman TITLE OF INVENTION: No. 644456el Juman G-Coupled Protein Receptor Kinases and Polymuc TITLE OF INVENTION: Encoding the Same LENGTH: 1662 TYPE: DNA ORGANISM: homo sapiens 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 2883.00 99.82% 99.82% 99.79% Mismatches: Indels: Length: Matches: Conservative:

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RESULT 3 US-09-738-894A-1 i Sequence 1, Application US/0973889 i Sequence 1, Application US/0973889 patent No. 6331423 i GENERAL INFORMATION: KARI et al i TITLE OF INVENTION: HIGGER I TITLE OF INVENTION: HOUSER: US/09. CURRENT FILING DATE: 2000-12-18 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FASTSEQ FOR WINDOWS Veri SEQ ID NO 1 SEQ ID NO 1 LENGTH: 1662 TYPE: DNA ORGANISM: Human US-09-738-894A-1 Alignment Scores: Pered. No.: SCORE: 2876.00 Percent Similarity: 99.64% Dest Local Similarity: 99.55% DB: US-10-044-205A-2 (1-553) x US-09-738- ON 1 MetValAspMetGlyAlaLeuAs ON 1 MetValAspMetGlyAlaLeuAs ON 1 MetValAspMetGlyAlaLeuAs ON 21 LysProSerAspCysAspSerLy DB 61 AAGCCCTCGGACTGCGACAGCAA	Db 1494 ATTTATGAAATGGTTGCTGGA Qy 401 GluAspLeuLysGlnArgThr

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GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
                                                                                                                                                                           AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG
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                                                                                                                 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG
                                                   | IleTyrGluMetValAlaGlyArgThrDroDheLysAspTyrLysGluLysValSerLys 400
                                                                                              ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
                                 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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CURRENT APPLICATION NUMBER: US/09/964,469
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GUEGLER, KAYL et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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                 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
                                                                                 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA
                                                                                                                                           ATCCTAATGGGAAAGGTAAGTTÄTTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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LENGTH: 1062
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Patent No. 6444456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/09/802,117
CURRENT APPLICATION NUMBER: US/09/802,117
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 60/188,449
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 5
COMMENCE OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: homo
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                                                                  LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
                                                                                                                                                 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg
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RESULT 6
US-09-738-894A-3
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000636
                                                                                                                                                             Sequence 3, Application US/09738894A Patent No. 6331423
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CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C
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; TYPE: DNA; ; ORGANISM: Human ; FEATURE:	Fast 3 36651	; PRIOR APPLICATION NUMBER: 09/738,894 ; PRIOR FILING DATE: 2000-12-18 ; NUMBER OF SEQ ID NOS: 4	PRIOR FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 60/208,331 PRIOR FILING DATE: 2000-06-01	RENCE: CL000636D PPLICATION NUMBE	ITITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ITITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES	·	US-09-964-469-3 ; Sequence 3, Application US/09964469 : Patert No 4572700	Db 4596 CCAGAGG 4602	348	4.	328 yAsnCysArgLeuSerAspLeuGlyLeuGlaValgluMartwsGlwGwGaArgAcCTCGG	QY 308 8GluLeuGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGl 328 Dh 4476 7G3ACTCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	4416 GGACATGAGCCGGC	Qy 288 uAspMetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHi 308	Db 4356 GAGCCTGATGATTGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCT 4415	268 tSerLeuMetAsnGlyGlyAspLeuLyspheHisTleTvrhenValClyTvrhenColl	CY 248 rProPheILeValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMe 268	4236 GAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGCAGGC	Qy 228 sLysLysClyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSe 248	The state of the s	4116 CAGTACCATCTAC	Qy 205ValCysAlava 208	Db 4056 CTTTCTCCAATGCCTAACATCTTTCCACCCACCTCCTTTTATCATCTCCACCTCTCTG 4115	Db 3996 AGGAGTATCGCACTGTAGTCCCCCACTTTTTCTTGAGAACACTTCTTATTTACAGCTACTC 4055	Qy 204 204	Db 3936 TCCTTGCCAACACTTGATATTTTCCTGTATTTTTTTTATGAAGGCCTGCCT	Оу 204 204	Db 3876 CCAAACTTTCCACATTTTTATTCCCACCAGCAATGCTTAAAGGTTTCGATTTTCTCCACA 3935

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3996 AGGAGTATCGCACTGTAGTCCCCACTTTTTCTTGAGAACACTTCTTATTTACAGCTACTC 4055	Oy 204 204 Db
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204 204	2736 AAGGGGGTAATGTTGCCTTTCTTTTTAAATCTCAGTTACTTAGAACTAATTTCAGCAC 2795
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3456 GCCCATTAATAGTGCCTCCCCATCCCTCTCCTCCTCCAGCCCTGACAACCACTAGTCCGC 3515	
204 204	Db 2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTTGGGAGCTGGCCGAGGAGGGACCC 2375 Qy
3396 AATGCAATGTTGGGTAAGCAACACCTCAATCTGGATCCAAGACACTCTCATCACCCCTGT 3455	
204 204	Db 2256 GAGCAGCAGCCGATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACGTTC 2315 Qy
4, 1	2196 GGGCTGCAGGGCTGCGCGGAAGCTCCGCCAWAAHGCTGTCCCTGAAAGCTTCCACACCCCCTGC 80
3276 ACCACTGTTGTGCCCCAGCTTTCTGTTTTTAAGTAATAAAAAATATTTCAGGTAAAATTTTG 3335	<u> </u>
	2136 AAGCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGCGTAGCCTGGCCC 2195
3216 AAGAAAGAAAGAAAGAAAGAAACACTTATCTTGAAGTAAGGTTGAGAACCTGTTTTGT 3275	21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
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207 3156 PAGATOGTGCCACTCCAGCCTGGGTGACAGAGCAAGACTCAAAAAAAA	1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
HCT LAGRINGA CARACTERISTICS	044-205A-2 (1-553) x US-09-964-469-3 (1-36651)
COMPOSED CONTROL AND ARCHAGA ATCACTTGAGCCTGGGGAGGTGGAGGTTGCAGTGAGCCC	Indes: 493 Gaps: 1
3036 TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGUI 3095	Score: 1528.00 Matches: 349 Percent Similarity: 41.40% Conservative: 0 Percent Similarity: 41.40% Migmarches: 1
204 204	Length:
2976 TGTGTGACAGAAGATCTCCGTTTCCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA 3035	
204 204	; INCATION: (1) (36651) ; LOCATION: (1) (36651) OTHER THROPHATION: n = A.T.C OF G
2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA 2975	Db

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Alignment Scores: Pred. No.:
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; ORGANISM: Homo sapiens
US-09-614-748A-7
                                Percent Similarity:
Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/614,748A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: PCT/US99/00663
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/071,199
PRIOR FILING DATE: 1998-01-12
                     Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09614748A Patent No. 6660474
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL TITLE OF INVENTION: HYPERTENSION
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FELDER, ROBIN A. APPLICANT: JOSE, PEDRO
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/098,279 PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                    ENGTH:
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                            1191 TIGAAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGT 1250
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337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
                                                   317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
                                                                                                                 297 SerAlaGlnIleAlaÇyşGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
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                                                                                                                                                   AAGTTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGGAGGAGGCCGTTTTCTAT
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DB:
143 ArgValAlaAlaValThrLeuArgLysAla------GluAlaMetAla 156
                                                                                                                                          123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142
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                                                                               -GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: A Method For Extracting Qua
TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 60
LENGTH: 2511
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 US-10-044-205A-2 (1-553) x US-09-417-197-60 (1-2511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 60, Application US/09417197
Patent No. 6518021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                      LOCATION: (1) .. (2508)
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NAME/KEY: CDS
                                                                                                                                                                                                                                      OTHER INFORMATION: Grk5-EGFP
                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                      TYPE: DNA
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 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal
                                                       SeraspLeuGlyLeuAlaValGluMetLysGlyGlyLysProileThrGlnArqAlaGly 352
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                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Ole THASTRUP, et al.

TITLE OF INVENTION: A Method for Extracting Quantitative Information Relating To An TITLE OF INVENTION: On A Cellular Response

FILE REFERENCE: 3759-0110P

CURRENT APPLICATION NUMBER: US/09/417,197

CURRENT FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SOFTWARE: PatentIn version 3.0

SEQ ID NO 42

LENGTH: 2529

TYPE: DNA

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/09417197 Patent No. 6518021
                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                  FEATURE:
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333 SerhspLeuGlyLeuhlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
                                                                                                                                                                                                             273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
                                                                                                                                                                                                                                                                                                                                                                       233 GluLysMethlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal 252
                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGly 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 AsplysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
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                                                                      ValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
                                                                                                               GCCTTGTTTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACC 1677
                                                                                                                                        ValllePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
                                                                                                                                                                                                                                                                                     SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
                                     GTCTACCGAGATCTGAAAACCTGAAAACATCCTGTTAGATGATTATGGCCCACATTAGGATC 1737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTACAGAAGCCGTGCAAAGAACTCTTTTCTGCCTGTGCACAGTCTGTCCACGAG---
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US-09-016-434-1298
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Patent No. 6500938
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                                                                                       ZIF: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION F
TITLE OF INVENTION: PATHWAY GENE
NUMBER OF SEQUENCES: 1490
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              COUNTRY:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1975 GTGTACTCCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACG 2031
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGERRINCE/DOCKET NUMBER: PA-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LENGTH: 2557 base pair
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            193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
                                                                                                                      173 AsplysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
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FILE REFERENCE: FELDER 3.9-001 CONT
CURRENT APPLICATION NUMBER: US/09/614,748A
CURRENT APPLICATION NUMBER: US/09/614,748A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: CT/US99/00663
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/071,199
PRIOR APPLICATION NUMBER: 60/071,199
PRIOR APPLICATION NUMBER: 60/071,199
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-08-28
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Best Local Similarity:
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US-09-614-748A-9
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SEQ ID NO 9
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ORGANISM: Homo sapiens
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261 CTCGAGAACATCGTGGCAACTCGCTGCTGCTGAAAGCGCGTCAAGGAGGATATGGCAAA 320
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TACCTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTA
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                                                                                                                                     ArgValAlaAlaValThrLeuArgLysAla-----
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US-09-614-748A-8
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GENERAL INFORMATION:
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APPLICANT: JOSE, PEDRO
TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: FELDER 3.9-001 CONT
CURRENT APPLICATION UNMERS: US/09/614,748A
CURRENT FILING DATE: 2000-07-12
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/071,199
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/098,279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIleGly 66
                                                                                                                                                                                                                                                               proPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGluArg
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TrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeu 197
                                                                                     LeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGln 177
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                                                                        TGGCAGAATGAGATGAATCCGGGTGTTTCAAAGACATCAAC 1736
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match: DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BENOVI
APPLICANT: PRIYA
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JEJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/076 FILING DATE: June 11, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
COMPUTER: IBM PS/2
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TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
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STATE:
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SOFTWARE: WORDPERFECT 5.1
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                                                                                                                                                                         46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle
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                                                            GGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGTCGCC 308
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TGCCTCCTGTACGAGATGATCACAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATC 1236
                                                                                                                                                                                                                                                                                  CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398
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RESULT 15
US-08-221-817-12
Percent Similarity:
Best Local Similarity:
                                                                                                         US-08-221-817-12
                                                   Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                          TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el
TITLE OF INVENTION: Kinase GRK6
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                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                FEATURE:
                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                            LOCATION:
                                                                                                                                               NAME/KEY:
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Conservative:
     Mismatches:
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DB: 10-044-205A-2 (1-553) x US-08-221-817-12 (1-2204) QY
PRACCH: 1 -044-205A-2 (1-553) x US-08 7 LeuAspAsnLeuIleAla 37 CTCGAGAACATCGTAGCG 27 SerLysGluLeuArgGlnLys 37 CTCGAGAGCTAGCGAAAGCAAG 46 AlaGluLeuArgGlnLys 157 GAAGAGCTGCGCTCAGC 66 GlyArgArgLeuPheArg 117 GGGCCCTTCTGGATGGGTTCCGA 86 PheLeuGluAspValGln ::: 217 GGCACGTAACGCAGAAT 86 PheLeuGluAspValGln ::: 217 GTCCTGGATGGGTGGCC 103 AspSerAlaLeuGlnGyValI 139 CGGCAGCTGGTGCAGACT 123 GlnProPheLeuSerGln 113 ThrGluGluGluArgValI 139 ThrGluGluGluArgValI 490 AGCGTGGCCCCTTTTGCCC 119 LysLeuPheGluMetGln 550 AAGTGGCTGGAAAGGCAGC 119 LysLeuPheGluMetGln 610 AAAGGTGGCTTAGAGAAAA 239 GluLysCylyPheGlyPheGlyGlu 610 AAAGGTGGCTAGAGAAAA 239 GluLysGluIleLeuGlu 191 LysClyGlyPheGlyFheGlyGlu 610 GAAAGCAAGAAGCTAGAAAAA 239 GluLysGluIleLeuGlu 191 LysClyGlyPheGlyFheGlyGlu 610 GAAAGCAAGAAGCTAGAAAAA 239 GluLysGluIleLeuGlu 191 LysClyGlyPheGlyGlu 610 GAGACCAAGAGCCCTTGGAGA 259 GluSerLysThrHisLeuC 259 GluSerLysThrHisLeuC 259 GluSerCAGAGACGCCCCTTTTGAGAGAAAA 259 GluSerLysThrHisLeuC 259 GluSerCAGAGACGCCCCTTTTGAGAGAAAA 259 GluSerLysThrHisLeuC 259 GluSerCAGAGACGCCCCTTTTGAGAGAAAA 259 GluSerCAGAGACGCCCCTTTTGAGAGAAAA 259 GluSerLysGluTleLeuGlu 1790 GAGACCAAGAGCGCCCTTTTTGAGAGAAAA 259 GluSerLysGluTleLeuGlu 1790 GAGACCAAGAGCGCCCCTTTTTGAGAGAAAA 259 GluSerCAGAGACGCCCCTTTTTGAGAGAAAA 259 GluSerCAGAGACGCCCTTTTTGAGAGAAAA 259 GluSerCAGAGAGCCCCCTTTTGAGAGAAAA 259 GLUSAGAGCAGAGCCCCTTTGAGAGAAAA 259 GLUSAGACCAAGAGCCCCCTTTTTGAGAGAAAA 259 GLUSAGACCAAGAGCCCCCTTTTGAGAGAAAACCAAGAGAGCAGAGCCCCTTTTGAGAGAAACCAAGAGAGCAGAGCCCCTTTTTGAGAGAACCAAGAGAGAG
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PRACCH: 1 42.85% 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
12.85% -044-205A-2 (1-553) x US-08-221-81
MACCH: 12.85% 142.85% 1 LeuAspAsnLeuIleAlaAsnTi :::: 37 CTCGAGAACATCGTAGCGAACAC 27 SerLysGluLeuGlnArgArg
PMACCH: 1 -044-205A-2 (1-553) x US-08-221- 7 LeuAspAsnLeuIleAlaAsnTh :::: :::: 37 CTCGAGACACTCGTAGCGAACAC 27 SerLysGluLeuGlnArgArg 46 AlaGluLeuArgGnLysLeuSe
42.85% 4-205A-2 (1-553) x US-08-221- 7 LeuAspAsnLeuIleAlaAsnTh :::: 37 CTCGAGAACATCGTAGCGAACAC 27 SerLysGluLeuGlnArgArg
42.85% 42.85% 42.205A-2 (1-553) x US-08-221- 7 LeuAspAsnLeuIleAlaAsnTH
MACCH: 1 2.85% 1 -044-205A-2 (1-553) x US-08-221- 7 LeuAspAsnLeuIleAlaAsnTh :::: ::: 37 CTCGAGAACATCGTAGCGAACAC 27 SerLysGluLeuGlnArgArg 97 CGCAAAGGCAAAAGCAAAGAAATG 46 AlaGluLeuArgGlnLysLeuSe 157 GAAGAGCTGCGGCTCAGCCTCGA 66 GlyArgArgLeuPheArgAspPh 217 GGGCGCTGCTGTTCCGAGAGTT 86 PheLeuGluAspValGlnAsnTr ::: 86 PheLeuGluAspTaGLGAGAGTT
MACCH: 1 2.85% 1 -044-205A-2 (1-553) x US-08-221- 7 LeuAspAsnLeuIleAlaAsnTh :::: ::: 37 CTCGAGAACATCGTAGCGAACAC 27 SerLysGluLeuGlnArgArg 97 CGCAAAGGCAAAAGCAAGAATG 46 AlaGluLeuArgGlnLysLeuSe 157 GAAGAGCTGCGGCTCAGCCTCGA 66 GlyArgArgLeuPheArgAspPh ::: 217 GGGCGCCTGCTGTCCGAGAGTT
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CAGAACGAGATGGTGGAGACCGAGTGCTTCCAAGAGCTGAAT 1605		GAGCCTACCGACCAGGACTTCTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGG 1563		ATTTACTGCAAGGATGTTCTGGAACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTG 1503	ValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPhe 497	AACTTCAAGCGGCTGGGAGCTGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCC 1443		CTGGGGTGTCGTGGGGGCAGTGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTG 1383		TTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGC 1323		AAGCGGAAGGAGTGGAGCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGC 1263	SerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsn 418	TGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATC 1206	CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398			1030 GTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCT 1089	ValGlumethysGlyGlyLysProlleThrGlnArgAlaGlyThrAsnGlyTyrMetAla 358

Search completed: August 13, 2004, 21:12:55 Job time : 149 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

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13: /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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	989,	Sequence 273, App) H	2 5					Seguence 482 Ann	٦	1 1	1, 1	2 0	Tride 'ca company	Segmence 25 Appl	45 Apr		_	Sequence 2, Appli	Sequence 1, Appli			_	•					20		•

ALIGNMENTS

RESULT 1 US-10-044-205A-1

Qy 61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA	Qy 1 GACCCTAAGATGAAGGGACCTCACTATAGGGCTCGAGGGGCCCCCGGGCAGGTGCTTTC	Query Match 100.0%; Score 2198; DB 14; Length 2198; Best Local Similarity 100.0%; Pred. No. 0; Matches 2198; Conservative 0; Mismatches 0; Indels 0; G	Sequence 1, Application US/10044205A Publication No. US20020123464A1 GENERAL INFORMATION: APPLICANT: KAPELLER-LIBERMANN, ROSANA APPLICANT: BANDARU, Rajasekhar ITILE OF INVENTION: 69087, 15921, and 15418, Methods and Compositions of Human Proteir ITILE OF INVENTION: Uses Thereof FILE REFERENCE: 10147-52U1 CURRENT APPLICATION NUMBER: US/10/044,205A CURRENT FILING DATE: 2002-04-19 PRIOR APPLICATION NUMBER: US 60/242,428 PRIOR FILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: US 60/241,884 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: US 60/241,884 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: US 60/241,887 PRIOR PRILING DATE: 2000-10-20 SOFTWARE: Patentin version 3.1 SEQ ID NO 1 LENGTH: 2198 TYPE: DNA CRGANISM: Homo sapiens
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	2161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTGA 2198	161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTG	ACATTTATTTTTTTTTTTTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCA 21	TAGAACACATTTTATTTTCTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCA 210	041 AATCAGTTAGGAGGGACATCACAACCACCACAAACAATICAAAAGACACAGGCAAAGCACAGGCAAAACAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAATICAAAAGACAAATICAAAAGACAAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAGACAATICAAAAAGAACAATICAAAAAGACAATICAAAAAGACAATICAAAAAGAAAAAAAAAA		GGGCT 204	981 GAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAAATGAGGGCT 204	921 CATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAG	921 CATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAG 198	.861 CGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGGGTAATT 19	1 CGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGGGTAATT 192	TCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAA 186	801 TCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAA 186	741 CTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGT 180	CTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGT 180	681 CTGGCCTAATTGAACCCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCCAAAGACATCG 174	681 CTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCG 174	621 AGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAG 1	21 AGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAG 168	162	61 AAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCACAGAAA 162	.501 AGCAAAGAACTCTGCAAGACGAGGTCAAATTTCCAGCATGATAACTTCACAGAGGAAGCAA 156	501 AGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAA 1	41 TGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAAGGTCAGTAAAGAGGA	441 Teerre	381 AAAAGG	381 AAAAGGTAAG	1321 GCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGG 1380	.321 GCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGG 138	1261 TGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTG 1320	N	1201 TGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTC 1260	σn.

RESULT 2
US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1

Qy 835 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTTGGGGAAAGGTGGTT 894	775 838	715 778	QY 655 CGCAACCCTTCCTCAGCCAGGCGTGGCCACCAAGTGCCAAGCAGCACCACTGAGGAAG 714	Qy 595 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 654	Qy 535 AGECGGCAACCTTCCTAGAGGACGTGCAGAACTTGGGAGCTGGCCGAGGAGGAGGACCCACCA 594	Qy 475 AGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 534	QY 415 TGCAGGGCTGCGCGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGGCCTGTGTGAGGC 474	355 418	Qy 295 TGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 354	QY 235 CCAGCAGCCTCCAGCCTCTTGTGCTTTCCCTGGGAGTGCCCCCGTGCCTCAGCCATGG 294	QY 175 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 234	Query Match 91.4*; Score 2008.8; DB 15; Length 2249; Best Local Similarity 99.9*; Pred. No. 0; Mismatches 2010; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	; TYPE: DNA; ORGANISM: homo sapiens US-10-217-745-5	; NUMBER OF SEQ ID NOS: 5 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 5 ; LENGTH: 2249	CURKENT APPLICATION NUMBER: US/10/217,745 CURRENT FILING DATE: 2002-08-12 PRIOR APPLICATION NUMBER: US/09/802,117 PRIOR FILING DATE: 2001-03-08	; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases; TITLE OF INVENTION: Polynuclectides; TITLE OF INVENTION: Encoding the Same ; FILE REFERENCE: LEX-0147-USA	; GENERAL INFORMATION: ; APPLICANT: Walke, D. Wade ; APPLICANT: Wilganowski, Nathaniel L. ; APPLICANT: Turner, C. Alexander Tr
- V	Q dd	A da	Db Qy	dd VQ	da Qy	Qy da	Db Qy	Оу	Qy Db	Qy db	Db Qy	Ωу	Qy Db	Qγ	Db V	ar II	
1915 GTAATTCATCCAAGTCTGGCGTGTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 1974	TAGAAJ TAGAAJ	AGCAGI AGCAGI	1735 ACATCGCTGAAAITGATGATTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1794 	1675 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1734 	1615 GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCC 1674 	1555 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1614 	1495 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1554	1435 ATGAA 1498 ATGAA	1375 TAATG 1438 TAATG	1315 1378	1255 TGCT	1195 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG	1135 ACGT 1198 ACGT	1075 CCCA 1138 CCCA	Y 1015 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1074	955 TGGA 1018 TGGA	b 958 TIGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 1017

CURRENT APPLICATION NUMBER: US/10/044,205A CURRENT PILING DATE: 2000-04-19 PRIOR APPLICATION NUMBER: US 60/241,849 PRIOR APPLICATION NUMBER: US 60/241,849 PRIOR APPLICATION NUMBER: US 60/241,877 PRIOR PILING DATE: 2000-10-20 NUMBER OF SEQ 1D NOS: 44 SOFTWARE: PARENTH Version 3.1 SEQ 1D NO 3 LENGTH: 1699 TYPE: DAN ORGANISM: Homo sapiens US-10-044-205A-3 JACGUCTICGACHTGGGGGCCCTTGGACAACCTGCCCAACCGCCTACCTGCACGCCCGG 350 PRIOR PILING DATE: 2001-10-20 PRIOR	RESULT 3 US-10-044-205A-3 US-10-044-205A-3 Sequence 3, Application US/10044205A Publication No. US20020123464A1 PUBLICANT: KAPELLER-LIBERWANN, Rosana APPLICANT: MANDARU, Rajasekhar TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Proteintle Reference: 10147-5201 FILE REFERENCE: 10147-5201	Db 2038 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2097 Oy 2035 AGGGCTAATCAGTTAGGAGGGACATCACACCACAAACAATTCAAAAGACAGGCAAGCT 2094
5 5 <td>Q</td> <td>40 40 40 40 40 40 40 40 40 40 40 40 40 4</td>	Q	40 40 40 40 40 40 40 40 40 40 40 40 40 4
	951 AAACTGGACAAGAAGCGGCTGAAGAAGAAGGAGGCGCGAGAAGATGGCTCTCTTGGAAAAG 1010	711 GAAGAGGGAGTGGCTGCAGTGACGCTGCGCAAGAGCTTAGGCCATGCCTTTCTTGCAAGAG 770

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SEQ ID NO 45
: LENGTH: 1662
TYPE: DNA
ORGANISM: Homo sapiens
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                                     Query Match
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Publication No. US20040023242A1
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FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
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OTHER INFORMATION: Inc;
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GRETHER,
ELLIOTT,
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BURFORD, Neil
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BANDMAN, Olga
BOROWSKY, Mark L.
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Matches 1660; Conservative
1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCCAATGGTTACATGGCTCCTGAG 1370
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PRIOR APPLICATION NUMBER: PCT/US01/4923
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-29
PRIOR PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/261,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/261,535
PRIOR APPLICATION NUMBER: 60/269,622
PRIOR FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
CURRENT APPLICAT
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                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL COMPOUNDS
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 1662
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Best Local Similarity
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Sequence 1, Application US/10217745
Publication No. US20030004328A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030004328A1el Hu
TITLE OF INVENTION: Polynucleorides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX.0147-USA
                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-217-745-1
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                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                       PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: E------
                                                                                                                         CURRENT APPLICATION NUMBER: US/10/217,745
CURRENT FILING DATE: 2002-08-12
                         TYPE: DNA
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CURRENT APPLICATION NUMBER: 05/09/984,489 CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 60/208,331 PRIOR APPLICATION NUMBER: 60/738,894 PRIOR FILING DATE: 2000-12-18 PRIOR FILING DATE: 2000-12-18 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 1662 TYPE: DNA ORGANISM: Human US-09-964-469-1 Query Match Best Local Similarity 99.8%; Pred. No. 0;	RESULT 7 US-09-964-469-1 J. Sequence 1, Application US/09964469 Sequence 1,	OY 1851 ATTATAGANACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACTTGAGGTTGTGAG 1910	1731 AAAGACATCGCTGAAATTGATGATTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA	ACATCATTTCTTT	1491 1201 1551	Db 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGAG 1020 Qy 1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370 Qy 1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370 Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080 Qy 1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430 Qy 1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140 Db 1081 ATCTATGAAATGGTTAGCTTGTCTGTGAACGACTAAAGGTCAGTAAA 1490 Qy 1431 ATTTATGAAATGGTTGCTGGTGCAGCACCATTCAAAGGATAAAGGTCAGTAAA 1490 1141 ATTTATGAAATGGTTGCTGGTCGTGCAACGACCATTCAAAGGATAAAGGTCAGTAAA 1200
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LENGTH: 1662
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: 09/964,469
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILING DATE: 2000-06-01
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APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL000635DIV2
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                                                                            Query Match 75.4%;
Best Local Similarity 99.8%;
                                                               Matches 1659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10425962
Publication No. US20030180786A1
                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0;
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                                                                   APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine B.
TITLE OF INVENTION: Proteins and Nucleic Acids
FILE REFERENCE: 21402-258
                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
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Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
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Shimkets, Richard
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Grosse, William M.
Alsobrook II, John P.
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LENGTH: 1701
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PRIOR FILING DATE: 2001-02-07
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PRIOR APPLICATION NUMBER: 60/267,459
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Publication No. US20030004328A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: TUTHEY, C. Alexander Jr.
TITLE OF INVENTION: BOOGLOGOSOA328A1el Hur
TITLE OF INVENTION: Boogling the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/10/217,745
CURRENT APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
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US-10-217-745-3
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LENGTH: 1062
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Best Local Similarity 99.8%;
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Pred. No. 1.7e-308;
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PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILING DATE: 2000-06-01
PRIOR PRILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36651
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                                                                                                                                                                                               unery match 39.5%;
Best Local Similarity 95.1%;
Matches one 7----
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00636DIV
CURRENT APPLICATION NUMBER: US/09/964,469
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
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Pred. No. 1.1e-252;
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SEQ ID NO 2
LENCTH: 2848
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020034767A1
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TITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G

TITLE OF INVENTION: Receptor Kinases GRK5 and GRK6

FILE REFERENCE: JEFF-0118-DIV

CURRENT APPLICATION NUMBER: US/09/851,686

CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: US 08/464,954

PRIOR PILING DATE: 1955-06-06

PRIOR PILING DATE: 1955-06-06

PRIOR PILING DATE: 1953-06-11
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CGAGTGCTTCCAAGAGCTGAATGTC
                                     GGGACTGTTTGAGGAACTGAATGAC 1886
                                                                            CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615
                                                                                                                 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC
                                                                                                                                                           GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGCAGTT
                                                                                                                                                                                      TGAAATTGATGATTTCTCTGAGGTTCGGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT
                                                                                                                                                                                                                                        TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGGTCT 1495
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APPLICANT: Carter, Kenneth
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-13-01
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Best Local Similarity 56.2%;
Matches 890; Conservative
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LENGTH: 2848
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Ebner, Reinhard
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                                                                                                                                                                                                                                       GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA
                                                                                                                                                                                                                                                                                                                                         ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                       GOCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
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Pred. No. 4.2e-116;
0; Mismatches 683;
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1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435
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                                                                                                                                    CGAGTGCTTCCAAGAGCTGAATGTC 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
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CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10159856
Publication No. US20030228689A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6;
FILE REFERENCE: RTS-0365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.0%;
Best Local Similarity 56.2%;
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TYPE: DNA
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FEATURE:
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LOCATION: (63)...(1793)
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ALIGNMENTS

JOURNAL MEDLINE	TITLE	AUTHORS	REFERENCE	PUBMED	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION				DEFINITION	Locus
prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected characteristics.	Carninci, P., Shibata, Y., Havatsu. N., Sugahara v. chihata v.	Ν	10349636	99279253	Meth. Enzymol. 303, 19-44 (1999)	High-efficiency full-length cDNA cloning	Carninci, P. and Havashizaki, y.	1	Mammalia; Eutheria; Rodentia; Schurognathi, Muridae, Muri	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Fiiteleostomi.	Mus musculus	Mus musculus (house mouse)	HTC; CAP trapper.	AK051405.1 GI:26094516	AK051405	insert sequence.	RECEPTOR KINASE GRK6 (EC 2.7.1) homolog [Mus muscul]us] full	enriched library, clone:D130046K22 product; c booffern countries	Mus musculus 12 days embryo spinal ganglion chara press full 1	AK051405 2978 bp mRNA linear HTC 20-000-2003

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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Please visit our web site for further details.
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ACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAG 1467
                                                                                                                         CCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGG
                                                                      CTGTGGGCTACATGGCTCCAGAGGTGGTGAGG---
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Pred. No. 3.3e-77;
0; Mismatches 659;
                                                                                -AATGAGCGCTACACGTTCAGTCCTG
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REFERENCE
AUTHORS
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Direct Submission
Submitted (29-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                             Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                      Proc.
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BC057206.1 GI:34784381
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                                                                                                                                                                                                                                                        human and mouse cDNA sequences
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Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
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                                                                                                                                             CCGAGGAGGACCCACCAAAGACAGCGCGCCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTG
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Pred. No. 3.3e-72;
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Contact: nisc mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R. W., Bouffard, G. G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consortium (LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Priscilla Furth
                                                                 Touchman, J.W.,
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 123 Row: m Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7242151
This clone has the following problem: frame shifted.

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tissue_type="Mammary tumor. WAP-Tag model. 5 months old, /clone_lib="NCI_CGAP_Mam4" /lab_host="DH10B" note="Vector: pCMV-SPORT6" organism="Mus musculus"

Length 2989;

340 TGCAGGCCGGAAGCCCTCGGACTGCGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTA 396 145 CGGGCCGGGCGCGCTGCAGCCCATGGAGCTCGAGAACATCGTAGCGAACACGGTGCTAC 204 280 CGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACACCTGATCGCCAACACCGCCTACC GCCTGGCCCTGCCCGGGCTGCCAGGAGCTCCGCCAGAAGCTGTCCCTGAACT 456 CGAGACCTGAGCTGACCCGGTGTACTGCCTTCCTGGATGGGGTGTCTGAATATGAGGTGA ACCACAGCCTATGTGAGCGCCAGCCCATTGGGCGCCTGTTATTTCGTGAGTTCTGTGCTA 384 TCCACAGCCTGTGTGAGCAGCAGCCGATCGGTGGCCGCCTCTTCCGTGACTTCCTAGCCA 516 TGCTGCAGTTCCCCCATATCAGCCAGTGTGAGGAGCTTCGACTCAGCCTTGAGCGTGACT TCAAGGCCCGGGAAGGTGGTGGCGGAATCGCAAAGGCAAGAGCAAGAAATGGCGCCAGA 264 0; Mismatches 700; Indels 27; Gaps 444

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                                            1717 CAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTFG
                                                                                                     1501 AACTGAATTTCAAGCGGCTGGGAGCTGGCATGCTAGAGCCACCTTTTAAGCCTGATCCCC 1560
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                                                                                                               Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Pa
                                                                   NIH-MGC Project URL: ht
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                BC027597
2329 bp mRNA linear HTC 01-MAY-200 HOmo sapiens, Similar to G protein-coupled receptor kinase 2-like (Drosophila), clone IMAGE:4830673, mRNA.
                                                                                                           USA
                                                                                                                                                                                                    Strausberg, R.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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TGAAGTTGTCA----ATAATGAAAAGTATACGTTTAGTCCCGATTGGTGGGGACTTGGCTG
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Local Similarity
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885346
This clone has the following problem: frame shifted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
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TGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATG
                                                                   AGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTACATGGCACC
                                                                                                                                                                                     TGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGTTTGGCCAC
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/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              917 bp mRNA linear EST 13-MAY-2003
BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CSODL010YD11 3-PRIME, mRNA sequence.
BX392018
                                                                                                                                                                            cgi-bin/cluster.cgi?seq=CSOBAI046ZH12_CSO4416_l&cluster=3090.f.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAI046ZH12_CSO4416_1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                      Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3090.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    25-NORMALIZED"
                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
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                                   /clone="CSODLO10YD11"
/clone="CSODLO10YD11"
/cell type="B CELLS (RAMOS CELL LINE) COT 25-NORMAI
/cell lip="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
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                                                                                                                                                                                                                                               79 GAGGAAGAAGATCAAGCGGGAGGAGGTGGAGC
                                                                                Homo sapiens GPRK5 gene,
genomic survey sequence.
AY406080
AY406080.1 GI:39762054
                                                                   GSS
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                               Homo sapiens
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sapiens (human)

1721 bp VIRTUAL

DNA 1 TRANSCRIPT,

linear partial

GSS 15-DEC-2003 sequence,

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Local Similarity
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Pred. No. 5e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1721)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                         ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC
                                                                                                                                                                                                                                                                                                                  GCCTTTGAGAGCAAGACCCATCTCTGGCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                      CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 941
                                                                                                                                             GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 881
                                                                                                                                                                                ressectasarasecreressarsecrecarecareaacressearesperaressare 1230
                                                                                                                                                                                                                    AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGGGCCCTTGTTTAT 821
                                                                                                                                                                                                                                                     AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 1178
                                                                                                                                                                                                                                                                                           GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGGTGACCTG
                                                                                                                                                                                                                                                                                                                                                                  CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGGAAAGGGGAGTCCATGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          based on alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence was made by sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM2438"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 304.6; DB 49.5%; Pred. No. 2e-56;
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REFERENCE
AUTHORS
TITLE
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BQ057469
LOCUS
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KEYWORDS
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AGENCOURT 6739297 NIH MGC 99
5', mRNA sequence.
BODS7166
                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 1058]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ057469
BQ057469.1 GI:19816809
                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                             cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                              late: LLCM2064 row: j column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGTGAAGCGGGAGGAGGTCGACCGCCCGGGTCCTGGAGACGGAGGAGGTGTACTCCCAC 1178
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                                                                                                                                        quality sequence stop: 631.
Location/Qualifiers
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="tanc:9606"
/clone="IMAGE:5813090"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp mRNA line
Homo sapiens cDNA
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cDNA clone
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e IMAGE:5813090
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1169 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCATGAACTCGGCATCGT 1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        929 ТGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAGAAGCTGGCGA
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BQ061148 1019 bp mRNA linear EST 02-APR-200.
AGENCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGGAGGTATGTGCCGTCCAGGTGAAAAAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT
                                                                                                                                                                                                                                                             CTGGTGGGCGCTCGGCTCCTGTACGAGATGATCGCAAGCCAGTCGCCCTTCCAGCA 721
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/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: lymph; Vector: potB7; Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size G.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript ITRI (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 300.2; DB 1
Pred. No. 1.7e-55;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTÇAGAGTGCTGGGGAAAGGTGGTTTTGGGGGAGGTATGTGCCGTCCAGGTGAAAAAACAC 928
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                                                                                                                                        TCTGGCCTATGCCTTTGAGAGCAAGACCATCTCTGCCTTGTCATGAGCCTGATGAATGG 1108
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                                                                                                      CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG
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                                                                                                                                                                                                                                                   GAAGAIGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGGAGCCCTTTCATTGTCTC 1048
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/tissue_type="lymphoma, cell line"
/lab host="PH10B (phage-resistant)"
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/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI, Site_2: Note: following Site_2: Note: pot site_2: Note: pot site_2: Note: pot site_2: Note: this is a NIH_MGC
II RT (Life Technologies). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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Conservative

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Similarity

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RESULT 8 BQ061148

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SCCTTCTACGACAAGTTTCTG 81	Query Match 13.4%; Score 295; DB 29; Length 1721; Best Local Similarity 49.0%; Pred, No. 2.6e-54; Matches 553; Conservative 0; Mismatches 567; Indels 9; Gaps 3;	ļ	/gen /loc	/or /db	Inls sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers source 1. 1721	AL Submitted Rockville,	AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams M. D. and Gracilla.			M Mus muscul Eukaryota; Mammalia; 1 (bases		z	į	Qy 1469 TTACAAGGAAAAGGTCA 1485 Db 722 GAGGAAGAAGAATCH 720	Db 662 CTGGTGGGCGCTCGGCTGCCTCTGTACGAGATCGAGCAGCCAGTCCAGCA 721	CTICGTTTCCCATCCCATCCCATCCATCCATCCATCCATCCAT	L	Db 485 GTACAGGGACCTGAAGACCCGAGAATGTGCTTCTGATGACCTCGGCAACTGCAGGTTATC 1288	425		Db 365 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCT
Qy 1836 GCATGGCAGGAAGAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1884	Db 1416 NININININININININININININININININININI	1356 NNNNNN	1716	2y 1656 ACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCT 1715	Db 1236 CAGAGGCTGGGCCAGGAGGAGGGGGGGGGGGGGGGGGGG	1176	QY 1479 AAGGTCAGTAAAGAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCCAGCAT 1538	1419 1059	1359 1002	1299 CTGGCC 942 CTGGCC	1239 882	1179 822	762	Db 702 GCCTATGAAACCAAAGATGCACTATGCTGGTTCTGAACCAATATGAAATGGTGAACCATTATGCTGAACCAATATGAAATGGTGAACCATTATGAAACGATGAAACGATGAAACGAAACAATGATGAAAACGAAACAATGAAAACAAAC	1059 GCCTT	QY 999 CTCTTGGAAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 1058	582	Qy 879 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 938	819	Db 402 TACTTGAAGGGAGACCCCTTCCACGAGTACCTGGATAGCATGTATTTTGACCGTTTTCTG 461	

RESULT 10 BU526699

DEFINITION

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1476 NNNNNNNNNNNNNNNATGATAGAAACAGAATGTTTCAAGGAGCTGAATG 1524

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Mammalia; Eutheria; Primates;
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //tissus_type="epidermoid carcinoma, cell line"
//lab host="DH10B (phage-resistant)"
//clone lib="NHH MCC 101"
//clone lib="NHH MCC 101"
//clone="Organ: lung; "Vector: pOTB7; Site_1: EcoR1; Site_2:
//note="Organ: lung; "Vector: pOTB7; Site_1: EcoR1; Site_2: pOTB7; Site_1: potentially site_2:
//note="Organ: lung; Potentially site_1: potentially site_2: potentially 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:9606"
/clone="IMAGE:6536408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269;
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1419 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1359 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903 bp mRNA linear EST 03-SEP-200;
AGENCOURT 8728162 NIH MGC 47 Homo sapiens cDNA clone IMAGE:6339126
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM2533 row: h column: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCTCCAGAGGTCC---TGAAACACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 635.
Location/Qualifiers
/clone_lib="NIH_MGC_4/"
/clone_lib="NIH_MGC_4/"
/noce="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                                                                         /tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 47"
                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                     clone="IMAGE:6339126"
                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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ORIGIN

Matches 455;

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Local Match

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1479 AAGGTCA 1485
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                                                                                                                    K-EST0075316 S22SNU16n1 5', mRNA sequence. BM794145
          Homo sapiens (human)
                                                                            BM794145.1 GI:19142377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAGGAG 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1238
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Best Local Similarity 68.0%;
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.F.

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001
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Korea Research Institute of Bioscience & Biotechnology
Koeun-dong Yuseong-gu, Daejeon 305-333, South Korea
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TACGCCGCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGG
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Fax: +82-42-860-4409
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/cell_line="SNU-16"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCTGGGCAAAGGTGGCTTTGGGGAAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCTGGGGAAAGGTTGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAAACACTGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAAACACCTTCAGGCAATACCGA
                                                                                                                                                                                                                                                                                                                     TACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGAC 300
                                                                                                                                                                                                                                                                                                                                                                                   ĠĊĠĊŤĠŖŖĊĠŔĠŖŔĠĊŔĠŔŤĊĊŤĠĠŔĠŔŔŖĠŦĠĸŖĊŔĠŦŖĠĠŤŦŦĠŤŖĠŦĠŖĠĊŤĠĠĊĊ 240
                                                                                                                                                                                                                                                                                                                                                                                                               gereretregaaaageaaaretregagaagagereageagecetricarrereteregge 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ATGTATGCCTGCAAGAAGCTAGAGAAAAGCGGATCAAGAAGCGGAAAGGGGCAATG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGAAGATG
                          TACATGGCTCCTGAGATCCTAATGGA 1381
                                                                                                                            ĠĀĊĊŢĠĀĀĠĊĊĊĠĀĠĀĀĊĀŤĊŢŢĠĊŢĠĠĀŢĠĀĊĊĀĊĠĠŊĊĀĊĀŢĊĊĠĊĀŢĊŢĠŦĠĀĊĊŢĠ
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 TACATGGCTCCGGAGGTGGTGAAGAA 566
                                                             GGACTAGCTGTGCATGTGCCCGGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGT
                                                                                           GGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 272.2; DB 12;
Pred. No. 2.3e-49;
0; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                   420
                                                                                                                                      480
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REFERENCE AUTHORS TITLE COMMENT JOURNAL

VERSION KEYWORDS SOURCE DEFINITION ACCESSION ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1017) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene AGENCOURT 6862973 NIH MGC 99 Homo sapiens cDNA clone IMAGE:59201825', mRNA sequence. Homo sapiens BQ061150.1 GI:19884936 BQ061150 BQ061150 Unpublished (1999) Homo sapiens (human) 1017 bp mRNA linear EST 02-APR-2002 Collection (MGC)

RESULT 14 BQ061150

Tocus

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2083 row: h column: 07
High quality sequence stop: 697. Tissue Procurement: Lou Staudt Email: cgapbs-r@mail.nih.gov Contact: Robert Strausberg, Ph.D

information can be

FEATURES

Location/Qualifiers

source

EST 17-DEC-1999

888

834

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1711 ACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATGTTTCTCTGAGGTTCGGG 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1414 TTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1114 ACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGGTGATCT 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            994 TGGCTCTTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGG 1053
                                                                                                                                                                                                                                                   CAGAGCAACGCTTAGGAAGCAGAGAAAA---GTCTGATGATCCCAGGAAACATCATTTCT 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                              TCAGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTTCCCTTCGTTCCAG
                                                                                                                                               TTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAG 1710
                                                                                                                                                                                                     CGAAGCAGAGGCTGGCTGCCAGGAGGAGGGGGGCTGCAGAGGTCAAGAGACACCCCTTCT 654
                                                                                                                                                                                                                                                                                                      ACTCCCACAAGTTCTCCGAGGAGGCCAAGTCCGATCTGCAAGATGCTGCTCACGAAAGATG 594
                                                                                                                                                                                                                                                                                                                                                      AGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAAC 1593
                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGAAGGTGAAGCGGGAGGAGGTGGACCGGCCGGGTCCTGGAGACGGAGG---AGGTGT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCC 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTACATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATCCTATCCTGTGGACTGGT 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGCTTGGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGGGGCCGGGTGGGCACTGTTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGATCTGAĀACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGGGCCTTGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATC 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript I. RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH108 (phage_resistant)"
/clone_lib="MHH_MGC_99"
/clone_lib="WHH_MGC_99"
/clone="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5920182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 272.2; DB 1
Pred. No. 2.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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                                                                                                   714
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                   879
                                                                                                                    651
                                                                                                                                                                    819
                                                                                                                                                                                                                                                                           759.
                                                                                                                                                                                                                                                                                                                              439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 715 ACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGGTGAAG 774
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALI34968

815 bp mRNA linear EST 17-DEC-1
wd17a07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2328372 3' similar to gb:L15388 G PROTEIN-COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
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AI934968.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE GRK5 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI934968
                                                                                                                                                                                                       TACTTGAGGGGAGAACCATCCCACGAATATCTGGACAGCATGTTTTNTGACCGCTTTCTC 652
ĊŦŖĠĠŖŔŔĠĠĠĠĠĊŢŦĊĠĠĠŢŔĠĠŤĊŦĠŦĠĊĊŦĠĊĊŔĠĠŦŦĊĠĠĠĊŔĊĠĠĠŢŔŊŖŔŦĠ
                                        CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAAACACTGGGAAGATG 938
                                                                                                                                                    CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG
                                                                                                                                                                                                                                                           TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
                                                                                                         CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAANACACTTTCAGGCAGTATCGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATCCCATGNGCAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTATAGCATGGCAGGAAGTATTATAGAAACCGGACTGTTTTGAGGAACTGAATG 1884
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               /Cloue lib="Soares NFL T GBC S1"
//Cloue lib="Soares NFL State 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.B. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
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Search completed: August 13, 2004, 18:41:48 Job time : 3859.13 secs

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US-09-964-469-3
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US-09-808-21-817-12
US-08-454-439-12
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SEQ ID NO 5
LENGTH: 2249
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PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 5
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CURRENT FILING DATE: 2001-03-08
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polymuc
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
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ORGANISM: homo
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ALIGNMENTS

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Query	Query Match 91.4%; Score 2008.8; DB 4; Length 2249; Best Local Similarity 99 9%. Prod No 0.
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뮹	238 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 297
Ş	235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 294
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Ş	295 TGGACATGGGGGCCCTGGACACCTGATGGCCAACACGCCTACCTGCAGGCCCGGAAGC 354
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γ	475 AGCAGCCCATCGGTCGCCCCCCTTCCCTTGCCTAGCCACAGTGCCCACGTTCCGCA 534
뮹	538 AGCAGCCCATCGGCCGCCTCTTCCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 597

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                     AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1614
                                                                                                   ATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1554
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                                                                             ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG
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                                                            CACTACTAGAACACATTTTATTTTCTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG
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                                             CACTACTAGAACACATTTTATTTTTTTTTTTTTCTTTCATAAAGATGAGTAAAGTCTCAG
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Sequence 1, Application US/09802117

Sequence 1, Application US/09802117

Patent No. 6444456

GENERAL INFORMATION:

APPLICANT: Wilganowski, Nathaniel L.

APPLICANT: Wilganowski, Nathaniel L.

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: Encoding the Same

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: LEX-0147-USA

CURRENT APPLICATION NUMBER: US/09/802,117

CURRENT APPLICATION NUMBER: US/09/802,117

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 60/188,449

PRIOR APPLICATION OUNDER: US 60/188,449

PRIOR APPLICATION DATE: 2000-03-10

NUMBER OF ESC ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

TENGRA: 1662
                               8
                                                                                                                                                                           US-09-802-117-1
                                                                                    Matches
                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                             LENGTH: 1662
TYPE: DNA
ORGANISM: homo sapiens
                      291 ATGGTGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG
ب
ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG
                                                                                      Conservative
                                                                                                      75.5%;
99.8%;
                                                                                      Score 1658.4;
Pred. No. 0;
1; Mismatches
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         ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA
                                                                                         ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTTGCCATGGGATGCAGC
                                                                                                                                                                  ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
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                                                                   ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTTGCCATGGGATGCAGC
                                                                                                                                              ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PRO
TITLE OF INVENTION: ACID MOLECULES ENCODING:
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000636
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 1
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Patent No. 6331423
                                                                                                                                                                                                                                                                                         Matches 1659; Conservative
                                                                                                                                                                                                                                                                                                           Query Match 75.4%;
Best Local Similarity 99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1662
TYPE: DNA
ORGANISM: Human
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GAGCAGCAGCCCATCGGTCGCCCCCTCTTCCCTGACTTCCTAGCCACAGTGCCCACGTTC
                                                                             GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT
                                                                                                                                                            AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC
                                                       GGGCTGCAGGGCTGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT
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ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
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                  GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GUECLER, KAY1 et al
APPLICANT: GUECLER, KAY1 et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0635DIV
CURRENT APPLICATION UNMERE: US/09/964,469
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1662
                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Human US-09-964-469-1
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Best Local Similarity
Matches 1659; Conserv
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Best Local Similarity
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/09/802,117
CURRENT FILING DATE: 2001-03-08
CURRENT FILING DATE: 2001-03-08
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                                  US-09-738-894A-3
                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09738894A Patent No. 6331423 GENERAL INFORMATION:
                                                                                                                                                        NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
Query Match
                                                                                                                                                                                                      APPLICANT: GUEGLER, KAT et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOGGS6
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C
                                                                                                              TYPE: DNA
ORGANISM: Human
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; Sequence 3, Application US/09964469
; Patent No. 6579709
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Best Local :
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
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LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA
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                                                         GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCCGCAAC
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Pred. No. 1.8e-203;
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US-08-464-954A-2
                                                                          Matches 891;
                                                                                                            Query Match
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                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/0 FILING DATE: June 11, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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APPLICANT: PRIYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                   NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JE
                                                                                                                                                                                                STRANDEDNESS:
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STATE:
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                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US FILING DATE: Herewith
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SOFTWARE: WORDPERFECT 5.1
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Woodland Falls Corporate Park
210 Lake Drive East, Suite 20
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Pred. No. 1.1e-93;
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GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTGTACGAGAT 1195
                                           AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
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US-08-221-817-12
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GENERAL INFORMATION:
APPLICANT: Chantr FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPPLICATION UNMBER: 08/123,932
PILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 553151and, Greea E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981 TELEFAX: (312)
TELEX: 25-3856
INFORMATION FOR SEQ COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A NO. 5532151el G
TITLE OF INVENTION: Kinase GRK6 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300 TELEFAX: (312) 474-0448 CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: APPLICANT: NUMBER OF SEQUENCES: STREET: 6300 S CITY: Chicago COUNTRY: STATE: ADDRESSEE: APPLICATION NUMBER: SOFTWARE: 60606 Illinois 6300 Sears USA Gray, Patrick W. Chantry, David Patentin Release #1.0, Borun SEQ ID NO: Marshall, O'Toole, Tower, US/08/221,817 12: 233 Gerstein, South Wacker Drive Version Protein-Coupled Receptor Murray #1.25

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LENGTH: 2204 base pairs
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                                                    GTGCCTGGTGCTGACACTGATGAACGGGGGGGGCGACCTCAAGTTCCACATCTACCACATGGG
                                                                                                                   GAAAGTGAACAGTAGGTTTGTAGTGAGCCTTGGCCTATGAGACCAAGGACGCGCT
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                                 GGGACTGTTTGAGGAACTGAATGAC 1886
                                                                                                          CTTCAAAAACTTTIGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC
                                                                                                                                                                                     TGAPATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT
                                                                                                                                                                                                                                 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463
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                                                                                                                                                                                                                                                                                                                     TGCCCGCGAGGTGAAGGAGCACCCCCCTCTTTAAGAAGCTGGAACTTCAAGCGGCTGGGAGC
                                                                                                                                                                                                                                                                                                                                            GTCTGATGATCCCAGGAAACATCATTTCTTTAAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĢÇАААĞĞАСТСТĞСДАĞАÇĞАĞĞТСАДАЎТСОВӨСДТĞАТААСТТСАÇАĞДĞĞДАĞСАДА 1561
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                                                                         CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC
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RESULT 10
US-08-454-439-12
                                                                                                                                                                                                                                                                                                      Sequence 12, Appli
Patent No. 5591618
                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                                                               STREET: 65.
CITY: Chicago
CITY: Illinois
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                 COUNTRY: US
ZIP: 60606
                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                      Application US/08454439
                                                                                                                 6300 Sears Tower,
IBM PC compatible
                                                                                                                                                 Marshall,
                                                                                                                                                                                    24
                                                                                                                                                 O'Toole,
                                                                                                                   233
                                                                                                                 South Wacker Drive
                                                                                                                                               Gerstein,
                                                                                                                                               Murray
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US-08-454-439-12
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
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TYPE: nucleic acid
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ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
                                                                                                                                                                                                                                                                        GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG
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                                                     CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA
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                                                                                                                                                                ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC
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Pred. No. 2.5e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046
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; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Matches 890;
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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REGISTRATION NUMBER: 35,302
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DEDNESS: single
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                                                                                                                            GTGCGAAGAĞCTGCĞĞCTCAGCCTCGAĞCGTGACTATCACAĞCCTGTĞCĞAĞCGĞCACCG 212
                                                                                                                                                      ADATTCGCADAGGCADAGGADATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152
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Pred. No. 2.5e-93;
0; Mismatches 683;
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                                                                                                                                                                           GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
                                                         ACTITICCICACACCICCICCIGCAAACGCCTGCCGAACGCCTGGGGTGTCGTGGGGGGCAG 1343
                                                                                               AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAA 1621
                                                                                                                                      GCGGCTGGTGAAGGAGGTCCCCCGAGGAGTATTCCGAGCGCTTTTTCCCCGCAGGCCCGCTC 1283
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RESULT 13
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                                                                                           PRIOR APPLICATION DATA:
PRIOR MEDILICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
FILING DATE: 31-MAR-1994
                               APPLICATION NUMBER: 08/1:
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                         Illinois
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VENTION: A No. 5591618el G Protein-Coupled Receptor
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             5591618and, Greta E.
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                                                                   OMBER: 08/123,932
17 SEP 1993
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 474-0448
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Local Similarity 55.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                               GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 108:
                                                                                                                                                                                                                                            ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
                                                                                                                                                                                                                                                                                                                              GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
                                                                                                                                                                                                                                                                                                                                                                     ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488
                                                                     GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA
                                                                                                      GAAGCGGCTGAAGAAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 102
                                                                                                                                             GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA
                                                                                                                                                                                GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA
                                                                                                                                                                                                                                                                                             CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548
GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT
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Pred. No. 7.9e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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RESULT 14
PCT-US94-10487-21
                                                                                                                                                                                                                                                                                                                  Sequence 21, Application PC/TUS9410487 GENERAL INFORMATION:
                                                                                                                                                                                          APPLICANT: ICOS CULPCA.
APPLICANT: ICOS CULPCA.
TITLE OF INVENTION: Kinase GRK6
TITLE OF INVENTION: Kinase GRK6
TOTAL OF CHOMENCES: 24
                                                                                                                                                                        NUMBER OF SEQUENCES: 2.
                                                                                  STREET:
                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
COUNTRY: USA
                              STATE:
                                                                                                                 ADDRESSEE:
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6300 Sears Tower,
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VENTION: A Novel G Protein-Coupled Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1 CLASSIFICATION:
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Local Similarity 55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                         GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                                                                                                                                                                                          CTTCCTCAGCCAGGCGTGGCCACCAAGTGCCAAGCAGCCACCAGTGAGGAAGAAGAGCGAGT 721
                                                                                                                                                                                                                                                       TGGGCGTC---GGCTAATGCAGAATTTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA
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                                                                                                                                                                                                                                                                                                                                                                         TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG
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                  ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG
                                                                                                                                   AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGACCCTGCAAAG
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                                                                                                                                                         TGAAATTGATGATTTCTCTGAGGTTCGGGGGTTGGAATTTGATGACAAGATAAGCAGTT 1801
                                                                                                                 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505
                                                                                                                                                                                                                                                                                                                                       GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
                                                     CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
                                                                                                                                                                                                                                                                                              TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205
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                                                                                                                                                                                                                                                    TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTATGCCAAAGACATCGC 1741
                                                                                                                                                                                                                                                                                                                                                                                    ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325
                                                                                                                                                                                                                                                                                                                                                                                                                             AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
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US-08-221-817-10
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 05.
CITY: Chicago
CTATE: Illinois
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APPLICATION NUMBER: 08/1
FILING DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: No. 5532151and, REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1862 GGGACTGTTTGAGGAACTGAATGAC 1886
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482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
                                                                                                                                                                                                                                            305 GGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
                                                                                                                        93 AAATCGCAAAAGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152
                                                                       CTGCGCGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
                                        GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG
                                                                                                                                                              CGACAGCAAAG----AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
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ALIGNMENTS

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DB; ABG72173.
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/note= "The coding sequence given as SEQ ID
specifically claimed in Claim 1"
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Aaq87426 Ab161805

Adb53307 Abk49405

Primary r Rat GRK c Human GRK

disorders.

P-PSDB;

Novel isolated G protein coupled receptor kinase, 69087, nuclear signaling protein, 15821 or mitogen activated protein kinase phosphatase, 15418, useful for treating cellular proliferative or differentiative

Claim 1; Fig 1; 98pp; English

The present invention relates to the isolation of a novel human G protein coupled receptor (GPCR) kinase (GPCRK) designated 69087), a novel human runclear signalling protein designated 1521, and a novel human runclear signalling protein designated 1521, and a novel human mitogenactivated protein kinase (MAPK) phosphatase MAPKP designated 15418, and the polynucleotide sequences encoding them. The sequences such as convention are useful for treating and disgnosing disorders such as collular proliferative and differentiative disorders (e.g. haematopoietic cellular proliferative and differentiative disorders (e.g. haematopoietic cephilatic disorders, leukaemia, carcinoma, sarcoma or metastatic disorders). They are also useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive cepticals and pharmacogenomics), and in methods of treatment (e.g. trials and prophylactic). The sequences may also be used to screen public databases to identify other family members or related sequences. that bind the polypeptides. The polynucleotide sequences are useful for mapping their respective genes on a chromosome, identifying gene regions associated with cellular proliferative or differentiative disorders, and The polypeptide sequences are useful as immunogens to generate antibodies gene therapy. The present sequence encodes human GPCRK 69087

Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

Mismatches 0 DB 7; 0

Length 2198; Indels

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The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NHP (novel human protein) in the specification, which is shown in the sequence listing. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides
                                                                                                                                                                                                                                                                                             New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH78799 standard; cDNA; 2249 BP.
                                                                                                                                                                                                    Disclosure; Page 33-34; 34pp; English.
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888888888888888**%**& invention can be used to genetically engineer host cells to express GRK products in vivo. The nucleotide sequences of the invention are also useful in addressable arrays for identifying and characterising the temporal and tissue specific expression of a gene and in microarrays to screen collections of genetic material from patients who have a particular medical condition. The proteins of the invention are useful for generating antibodies, as reagents in diagnostic assays, for derived from the nucleotides of the invention are useful as hybridisation probes for screening libraries and assessing gene expression patterns. The nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRK expression. The nucleotides of the identifying other cellular gene products related to GRK, and as reagents in assays for screening for compounds that are useful in the treatment of biological or medical disorders/diseases

Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

Ś 밁 Ş Š 밁 ğ Ş 밁 8 맑 Ş 맑 δÃ 밁 Ś В Ş 뫄 8 멂 Ś 븅 맑 뮍 S Matches 2010; Query Match Best Local Similarity 895 838 718 595 865 535 538 475 478 415 418 355 358 295 298 238 175 898 835 775 778 715 655 658 235 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT CGCAACCCTTCCTCAGCCAGGCCTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGGTTCCGCA TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG AGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC AGCGAGTGGCTGCAGTGACGCTGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCCACCA AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCCTGCCCGGGC TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT <u>AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCCCACCA</u> Conservative 91.4%; 0; Mismatches Score 2008.8; Pred. No. 0; DB 4; 2 Indels Length 2249; 0; Gaps 297 954 594 477 417 234 894 837 654 657 597 534 537 474 414 354 357 957 897 834 777 714 717 294 774

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                                           CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG
                                                                                                                                        GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG
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Homo sapiens.	20
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gene; ss.	XX
myocardial infarction; ischaemic disease; hypertensive vascular disease;	KW
Alzheimer's disease; Parkinson's disease; congestive heart failure;	KW.
chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;	¥
central nervous system disorder; cardiovascular disorder; asthma; COPD;	¥
<pre>vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;</pre>	X
neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;	¥
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Human G protein-coupled receptor kinage encoding cDNA SEO TD NO:4	D R
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2155 TITTCACTGAGGGAAAAAGGAACACTCA 2186	Ş
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2098 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAACAA	В

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19-AUG-2002; 2002WO-EP009235

21-AUG-2001; 2001US-0313464P

(FARB) AG

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WPI; 2003-278669/27.

P-PSDB; ABP96709.

New G-protein coupled receptor kinase polypeptides and polynucleotides, useful in identifying modulators of the enzyme for treating cancer, diabetes, a central nervous system disorder, a cardiovascular disorder or

Claim 1; Fig 11; 129pp; English.

The present sequence encodes a human G protein-coupled receptor kinase (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective, nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and antiasthmatic activities, and can be used in gene therapy. (I) can be regulated to treat cancer, diabetes, a central nervous system (CNS) disorder (e.g. anxiety or mood disorders, Alzheimer's disease and Parkinson's disease), cardiovascular disorders (e.g. congestive heart failure, mycoardial infarction, ischaemic diseases of the heart or hypertensive vascular disease), asthma and chronic obstructive pulmonary disorder (COPD). GRK molecules are useful in screening for agents that regulate or decease the activity of a GRK. GRK sequences may also be used for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic

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	Qy 1107 GGGGG Db 901 GGGGG	Qy 1047 TCTCTO	Qy 987 GAGAAN	Qy 927 ACTGG	Qy 867 GAGTTO	Qy 807 GACAA Db 601 GACAA	Qy 747 GAGGC	Qy 687 AAGTG Db 481 AAGTG	Qy 627 TGTGC Db 421 TGTGC	Qy 567 TGGGA Db 361 TGGGA	Qy 507 TTCCT. Db 301 TTCCT.	Qy 447 TCCCT Db 241 TCCCT	Qy 387 CGGCG	Qy 327 AACAC Db 121 AACAC	Qy 267 TGGGA Db 61 TGGGA	Qy 207 CGTTG Db 1 CGTTG	Query Match Best Local Similarity Matches 1990; Conser	CC acid sequences XX SQ Sequence 3186
TTTTACTCGGCCCAGATAGCCTGT	GACCTCAAGTTCCACATCTACAAC GACCTCAAGTTCCACATCTACAAC	GCCTATGCCTTTGAGAGCAAGACC GCCTATGCCTTTGAGAGCAAGACC	atggctctctggaaaaggaaatc 	aagatigtatgcctgtaagaaactg 	agagtigctiggggaaaggtiggtttt 	HTTCTGCAGTGGAAACTCTTCGAG	ATGGCTTTCTTGCAAGAGCAGCCC	CAAGCAGCCACCACTGAGGAAGAG 	AGTGCCCCTGCCCGGGGAACCCG	CTGGCCGAGGAGGGACCCACCAAA	GCCACAGTGCCCACGTTCCGCAAG	hacticcacagccigigiagcag 	CGTAGCCTGGCCCTGCCCGGGCTC	GCCTACCTGCAGGCCCGGAAGCCC)TGCGCCCGTGCTCAGCCATGGT(POTCACCCGGGAAGGGAAAGCAGC	90.5%; Score 1988.8; nilarity 99.9%; Pred. No. 0; Conservative 0; Mismatches	sequences that encode the GRK enzyme ince 3186 BP; 857 A; 737 C; 784 G; 80
GTGATCTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATC	GGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGG	TCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAAT	GAGAAGATGGCTCTCTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTC	acteggaagatgtatgcctgtaagaaactggacaagaagcggctgaagaagaaaggtggc 	GAGTTCAGAGTGCTGGGGAAAAGTGGTTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAA 	GACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACC	GAGGCCATGGCTTTCTTGCAAGAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGAGGCCCATGGACAGCGCCTTCTACGAGATTTCGTGACCAGCGCCTTCTACGAGATTTCGTGACCAGCGCCTTCTACGAGATTTCGTGACCAGCGCCTTCTAC	AAGTGCCAAGCAGCCACCGCGCGGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCT	TGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACC	TGGAAGCTGGCCGAGGAGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCACT 	TTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAAC	TCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGAC	CGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGAGAGCTCCGCCAGAAGCTG	AACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAGCAAGAGAGCTGCAGCGG	TGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGGCCCTGGACAACCTGATCGCC	CGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCC	DB 7; Length 3186; 2; Indels 0;	me 808 T; 0 U; 0 Other;
	GCCGG 960	TGAAT 1106	TTGTC 1046	HIT HE PROPERTY OF THE PROPERT	далаас 926 далаас 720	TCACT 866 	TCTAC 806	 AGGCT 540	CCACC 686	SCACT 626	AGAAC 566 AGAAC 360	CGTGAC 506	AAGCTG 446 AAGCTG 240	AGCGG 386	ATCGCC 326 ATCGCC 120		Gaps 0;	
RE																		
RESULT	Db Qy	B &	, B &	o do Qy	db V2	Db Qy	dg VQ	D A	, B &	B 8	B 8	, B &	de dy	₽ &	S B &	B %	S B &	Db
SULT 4	Qy 2187 GGTTTATTTGA 2198 Db 1981 GGTTTATTTTGA 1992	OY 2127 TICTTCATAAAGAYGAGTAAAGTCTCAGTTTTCACTGAGGGCAGGGAAAAGGAACACTCA	1861	1801	1947 1741	1887	1827 1621	1767 CGGG	1501 CCAG	1647 TTCT 1441 TTCT	1381	1527 AAAT 1321 AAAT	1467 1261	1407 GACT 1201 GACT	1347	1081 TCTG	1227 GICT	961

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ADC39221

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23-MAY-2001;
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31-MAY-2001;
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03-DEC-2001;
03-DEC-2001;
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31-JUL-2001;
14-AUG-2001;
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10-SEP-2001;
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antilipemic;
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WPI; 2003-239445/23.
P-PSDB; ADC39222.
                                                       Gorman L, Guo X, Fernande
Patturajan M, Anderson DW,
Padigaru M, Rastelli L, SI
Edinger SR, Ellerman K;
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18-OCT-2001;
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21-MAY-2001;
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2001US-0293147P
2001US-0293147P
2001US-0294109P
2001US-0294110P
2001US-0294327P
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2001US-0304879P
2001US-0304879P
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; 2001US-0289087P.
; 2001US-0289817P.
                                                                       Kekuda R, Malyankar UM, Li L, Pena CEA, S
Juo X, Fernandes ER, Smithson G, Stone DJ,
Juo B, Fernandes ER, Peyman JA, Macde
Rastelli L, Shenoy SG, Gerlach VL, Shimke
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2001US-0291243P.
2001US-0292001P.
2001US-0292374P.
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one DJ, Zerhusen BD;
, Macdougall JR;
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       TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG
                       TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG
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                                                                                                                                                        CCTGCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCA
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New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,

The invention relates to new isolated NOVX polypeptides, the genes considered them or sequences having at least 95% identity to the amino acid cor nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NOVX corrections or alleviating pathology associated with NOVX corrections, preventing e.g. corrections, descriptions, a nonexia, wasting of preventing e.g. corrections, dyslipidemias, anorexia, wasting disorders, Alzheimer's disease, parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's corrections is disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's corrections is useful in gene therapy for treating the above conditions. These are also useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX genes of the

0 U; 0 Other;

CGGGAAGGGAAAGCAGCCAGCAGCCTCCAGCCCTCTTGTGCTTTTCCCTGGGAGTGCGCC CTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCTCCGCCAGAAGCTGTCCCTGAACTTC CTGCAGGCCCGGAAGCCCTCGGAACTGCGACAGCAAGAGAGCTGCAGCGGCGGCGGCGTAGC CCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTAC CCGTGCTCAGCCATGGTGGACATGGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTAC CGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCC CTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGCGTAGC DB 2 9; Indels Length 1821; 0; Gaps 458 398 338 180 120 60

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                          TGGCAGGAAGAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCT 1898
                                                                                                  TTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCA 1838
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TGGCAGGAAGAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCT
                                                                           TTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCA 1620
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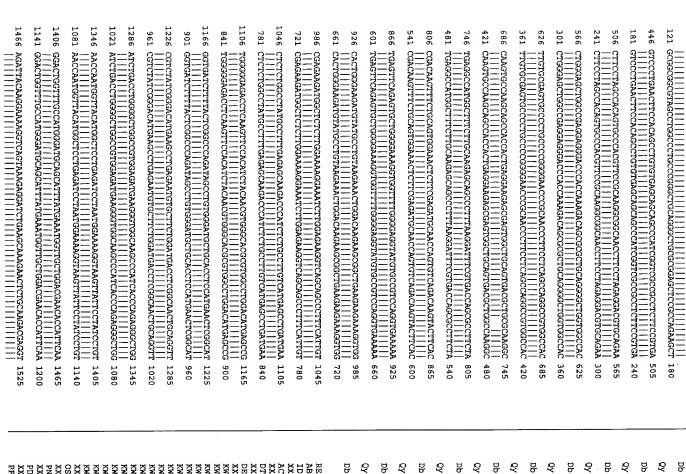
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386 GCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGAGCTCCGCCAGAAGCT

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                                                                                                                                                                                                            Query Match
Best Local S
Matches 1759
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel disease associated gene and its uses. The gene and its encoded protein are useful for diagnosis of and screening for drugs for heart diseases, cancers and omentopathy. The current sequence represents a human gene sequence relative to the
                                                                                                                                                                                                                                                                                                               Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel disease-associated gene of the RGS gene family and its product, applicable in diagnosis of and screening for drugs for heart diseases,
                                                                                                                                                                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 85-86; 96pp; Japanese.
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P-PSDB; ABP60079.
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                           CAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCG 385
                                                                                                   CTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCCTGGACAACCTGATCGC
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RESULT 6
ABQ86178
ID ABQ8

D ABQ86178 standard; DNA; k

1662 BP

ABQ86178;

10-SEP-2002 (first entry)

Novel human gene. SEQ ID 49

Whuman; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; who corropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; wound healing disorders; atherosclerosis; Parkinson's disease; Malzheimer's disease; autoimmune disorder; haematopoletic disorder; anfilammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; whyperpoliferation; systemic autoimmune disease; hyper-immunity; anewatological disease; metabolic disease; sperm dysfunction; developmental abnormality; gastrointestinal ulceration; neuropathy; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; cone photo- transduction deficiency; neurological disease; stroke; cone photo- transduction deficiency; neurological disease; stroke; trachea; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty; gene; ss.

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Homo sapiens.

PN WO200250105-A1

PD 27-JUN-2002

PF 17-DEC-2001; 2001WO-US049232.

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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The secretary sequences activity of polypeptides of the invention may be described as cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic opposition, immunosuppressive, haemostatic, antiinflammatory, antiarteriosclerotic, antiparkinsonian, pressive, haemostatic, antiinflammatory, antiarteriosclerotic, antiparkinsonian, and the sequences are sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ovulation disorders, diseases in the spinal cord, thyroid gland, heart, trachea, thymus, lymph node and muscular system, obesity, anorexia, growth abnormalities, and alleviation of precocious puberty. The sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1662 BP; 420 A; 411 C; 479 G; 352
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SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
CGCAAGGCGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGAGGACCC
                                                                           GAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCCACGTTC
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                                                    GAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC
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2000US-025704BP.

2001US-0260482P.

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2001US-0289622P.
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                     AGCAGAGAAAAGTCTGATGATCCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT
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2002-090207/12.

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23-JUN-2000;
30-JUN-2000;
07-JUL-2000;
13-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple solerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoathritis; cood pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative collitis; citrosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; citaract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout;
              Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalla A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
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                                                                                                                                                                   ); 2000US-0212073P.

); 2000US-0213467P.

); 2000US-0215651P.

); 2000US-021665P.

); 2000US-0218372P.

); 2000US-0228056P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Niemann-Pick's disease; gene therapy; ss.
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                                                          M, Greenwald SR;
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Query Match Best Local

Similarity

75.5%; 99.9%;

Score 1658.8; Pred. No.

DB 6;

Length 1662;

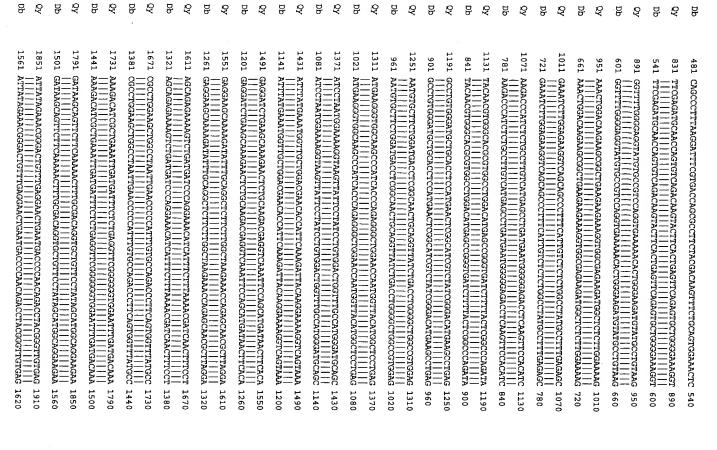
0

Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

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CC corresponding counse.

CC treating a disease or condition sosociated with decreased expression of CC PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with decreased expression of CC PKIN and a composition comprising PKIN antagonist is useful for treating CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); inmunne disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, CC atherosciences; gout, bronchitis, Crohn's disease, disbetes syndrome, cantoinmune thyroiditis, gout, bronchitis, Crohn's disease, disbetes syndrome, cantoinmune thyroiditis, gout, bronchitis, psoriasis, Reiter's syndrome, CC mellitus, multiple sclerosis, Good pasture's syndrome, cataves' disease, CC mellitus, multiple sclerosis, pancreatitis, psoriasis, Reiter's syndrome, CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, CC pacterial, parasitic, fungal, viral, protozoal and helminthic infections) CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, CC cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio CC vascular disease (arteriovenous fistula, hypotherision, vasculitis, CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid clischaemic heart disease, chronic bronchitis, lung tumours); lipid clischaemic feative liver, Fabry's disease, Niemann-Pick's disease, the compound and in gene therapy. The present sequence is human cropsological conditions of the compound and in gene therapy. The present sequence is human cropsological conditions of the compound and in gene therapy.
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human kinase PKIN proteins and their
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밁 S Ś 밁 S 밁 Ş 밁 Š 뮹 Ś 밁 S 밁 8 밁 Matches 1660; 421 361 301 591 241 531 181 471 121 411 291 651 351 771 711 61 Н ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410 CAGCCCTTTAAGGATTTCGTGACCACGCCCTTCTACGACAAGTTTCTGCAGTGGAAACTC GAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530 GGGCTGCAGGCTGCGCGAGCTCCGCCAGAAGCTGTCCCCTGAACTTCCACAGCCTGTGT GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCCTATGGCATGGCTTTCTTGCAAGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACCAAGTGCCAAGCAGCCACCACTGAG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGTGGCCGAGGAGGGACCC CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGTGGCCGAGGAGGGACCCC GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC GGGCTGCAGGGCTGCGCGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG Conservative 0; Mismatches 2 0 Gaps 420 710 360 650 300 590 240 180 470 120 60 480 830



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                                                                                                                                                                                                                                                                                                                                                                                                     Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7; GRK7; cone visual signalling; visual sensitivity; visual resolution; night blindness; colour blindness; Oguchi disease; Pineal gland activity; chronobiological desynchrony; depression; anxiety; memory loss; headache; mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
                                                                                                                                                                                                                                                  Bird TA,
                                                                                                                                                                                                                                                                               07-MAR-2001; 2001US-0274006P
                                                                                                                                                                                                                            P-PSDB; AAE28952.
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                antidepressant; analgesic; gene; ds
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                                                                                                                                                                                                                                                                                                                                            /product= "Human GRK7 protein"
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                                                                                                                                                                                                                                                 Mosley BA;
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Identifying compounds that alter inhibition of cone opsin kinase polypeptide activity for treating a conditions related to cone visual signaling, comprises mixing a compound with a cone opsin kinase and w inhibitory polypeptide with

Example 4; Page 45-46; 61pp; English.

CC Outpled receptor kinase 7; GRK7) and their corresponding polynucleotides. CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides. CC The invention further relates to a method of identifying compounds that CC alter the inhibition of GRK7 polypeptide activity which involves mixing a CC test compound with GRK7 protein and an inhibitory polypeptide and CC determining if the test compound alters the inhibition of GRK7 protein CC circating conditions related to cone visual signalling (e.g., night CC blindness, colour blindness, difficulty with colour vision, visual sensitivity, visual resolution or in adapting to changes in light CC blindness, Oguchi disease or dominant congenital stationary night CC blindness), Pineal gland activity (e.g., chromobiological desynchrony, CC depression, anxiety, mental fogginess, memory loss, headaches, fatigue, CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide activity is beneficial, e.g., decreased colour sensitivity or other cone photoreceptor-mediated diseases. The GRK7 proteins are also useful in the CC probes to screen for inherited defects in colour vision, circadian rhythm and vision resolution. They are also used as gene therapy tools for

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Best Local Sim:
Matches 1660;
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RAAH7877 1D
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RAH7 2D
RAH Human G-protein coupled receptor kinase 1 cDNA sequence 08-MAR-2002 AAH78797 standard; (first cDNA; entry) 1662 ВP

G-protein coupled receptor kinase; GRK; human; ss; gen drug screening; gene expression characterisation; NHP; novel human protein. Homo sapiens Location/Qualifiers 1. .1662

WO200168869-A2

/*tag= a /product= "G-protein coupled receptor kinase

20-SEP-2001

contenting libraries and assessing gene expression patterns. The nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRK expression. The nucleotides of the invention can be used to genetically engineer host cells to express GRK products in vivo. The nucleotide sequences of the invention are also useful in addressable arrays for identifying and characterising the temporal and tissue specific expression of a gene and in microarrays to screen collections of genetic material from patients who have a particular medical condition. The proteins of the invention are useful compensating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to GRK, and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders/diseases Matches 1659; Query Match The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NHP (novel human protein) in the specification, which is claimed in the invention. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides derived from the nucleotides of the invention are useful as hybridisation probes for New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological WPI; Sequence 1662 BP; 420 A; 410 C; 479 G; 352 T; 0 U; 1 Other; Claim 1; Page 30; 34pp; English. P-PSDB; AAG77815. 08-MAR-2001; Walke 10-MAR-2000; 2000US-0188449P (LEXI-) LEXICON GENETICS Local 591 361 301 241 181 471 411 291 711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 121 351 2001-570872/64. 61 ч Similarity ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCCGGGG 650 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGAGCCC 590 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACCAAGCGCAGCAGCACCACCACTGAG 710 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGCTGGCCGAGGAGGGACCC GAGCAGCAGCCATCGCTCGCCGCCTCTTCCGTGACTTCCTAGCCAACAGTGCCCACGTTC 530 ATGGTGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGGCTTACCTGCAGGCCCGG GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC **AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG** ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG GGGCTGCAGGGCTGCGGGAGCTCCGGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT GGGCTGCAGGGCTGCGCGAAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGGCCTGTGT 470 ATGGTGGACATGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG Wilganowski NL, Conservative 2001WO-US007500 75.5%; 99.8%; Mismatches Score 1658.4; Pred. No. 0; Turner CA; DB 4; 2; Indels Length 1662 and as reagents ٥, Gaps 300 240 420 360 180 120 60 0 뮍 Ś 뮹 Ś 밁 Ś 맑 Ş 밁 Ş 맑 Ş 8 문 밁 8 맑 Ş 밁 8 망 멂 Ś S 뮍 δ 밁 Ś 맑 밁 Ş 8 8 뮍 밁 1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1321 1611 1551 1201 1431 1081 1021 1191 1071 1131 1011 961 901 841 781 661 541 721 951 601 891 831 481 771 421 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC 1130 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA GAGGATCTGAAGCAAAGAACTCTGCAAGACGACGACGAAATTCCAGCATGATAACTTCACA ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG GCCTGTGGGATGCTGCACCTCCATGAACTCCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTTGGGAAGATGTATGCCTGTAAG CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC AGCAGAGAAAAGTCTGATGATCCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG AMACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT

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The invention relates to human kinase proteins that are related to G-CC protein coupled receptor kinase subfamily. Human kinase gene is located CC on chromosome 3. The kinase peptide and nucleic acid are useful in the CC development of human therapeutic and diagnostic compositions. The peptide CC valuable to the field of pharmaceutical development to identify and CC characterise modulators of the kinase. The proteins may also be used to CC raise antibodies or to elicit an immune response, as a reagent in assays CC designed to quantitatively determine levels of the protein in biological CC fluids and as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage CC fitssue differentiation or development or in a disease state). The CC kinase proteins are also useful for providing a target for diagnosing a CC disease or predisposition to disease mediated by the peptide. The nucleic acid molecules are useful for probes, primers, chemical intermediates and CC containing the gene regulatory regions of the nucleic acid molecules and cCC containing the gene regulatory regions of the mucleic acid molecules and cCC acid expression. The present sequence is human kinase cDNA expressed in CCC skins, germinal center B cells, colon, kidney and lung
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                                                                                                                                                                                                                                                                                          New isolated human kinase proteins and nucleic acids, useful as a major target for drug action and development, particularly for screening modulators of the kinase peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; kinase; G-protein coupled receptor kinase; tissue differentiation; chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
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18-DEC-2000; 2000US-00738894.
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(SUGE-) SUGEN INC
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CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel CC protein kinases have been identified as members of the tyrosine or serine/threonine kinases (PTK and STK) families. The polynucleotides CC encoding protein kinases and the polypeptides may be used in the CC prevention, diagnosis and treatment of diseases associated with CC inappropriate kinase expression. For example, they may be used to treat CC cancers (especially cancers of haematopoietic origin), cardiovascular CC immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. diseases (e.g. schizophrenia), neurodegenerative disorders (e.g. disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious CC disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for CC gene therapy and as DNA probes in diagnostic assays. The protein kinase CC against the protein kinases and in assays to identify modulators of nrorein kinase expression and activity
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Flanagan P,
                                    protein kinase expression and activity
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P-PSDB; AAU03502.
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Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

S Ś 밁 맑 Ş 문 Ś Query Match Best Local S Matches Local Similarity 1658; 471 121 411 351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGCGGCGTAGCCTGGCCCTGCCC 291 ATGGTGGACATGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 61 ш GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530 GGGCTGCAGGGCTGCGGAGGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT GGGCTGCAGGGCTGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG Conservative 75.3%; 99.8%; 0; Mismatches Score 1655.6; Pred. No. 0; DB 4; Length 1662; 4; Indels . . Gaps 180 120 410 60 350 0

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GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG

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AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACCAAGTGCCAAGCAGCCACCACTGAG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG

ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCCTGCCCCGGGG

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GAGCAGCAGCCCATCGCCCCCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC

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CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCCC

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Location/Qualifiers /*tag= .1662

/product= "G protein-coupled receptor kinase വ

WO2003018815-A2

06-MAR-2003

19-AUG-2002; 2002WO-EP009235

21-AUG-2001; 2001US-0313464P

(FARB) BAYER AG

Xiao Y;

WPI; 2003-278669/27.

P-PSDB; ABP96707

New G-protein coupled receptor kinase polypeptides and polynucleotides, useful in identifying modulators of the enzyme for treating cancer, diabetes, a central nervous system disorder, a cardiovascular disorder or

Claim 1; Fig 1; 129pp; English

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GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952

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The present sequence encodes a human G protein-coupled receptor kinase (CRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective, CC nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and CC antiasthmatic activities, and can be used in gene therapy. (I) can be CC regulated to treat cancer, diabetes, a central nervous system (CNS) CC disorder (e.g. anxiety or mood disorders, Alzheimer's disease and CC Parkinson's disease), cardiovascular disorders (e.g. congestive heart CC failure, myocardial infarction, ischaemic diseases of the heart or CC hypertensive vascular disease), asthma and chronic obstructive pulmonary CC disorder (COPD). GRK molecules are useful in screening for agents that CC regulate or decease the activity of a GRK. GRK sequences may also be used CC and abnormalities related to the presence of mutations in the nucleic acid sequences that encode the GRK enzyme

Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 1658; Conservative 75.3%; 99.8%; o ; Pred. No. 0; Score 1655.6; Mismatches BB 4 7; Length 1662; <u>..</u> Gaps

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Human; RGSNo9; heart disease; cancer; omentopathy; gene; Human RGSNo9 encoding DNA # SEQ ID ABZ56934 standard; DNA; 1191 BP 14-JUN-2002; 2002WO-JP005942 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1610 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550 GAGGGTAAITCAICCAAGTCIGGCGTGTGTTTGTTAITGTAA 1952 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490 GATAAGCAGTTCTTCAAAAACTTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG Location/Qualifiers
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                                                                      GAAATCTTGGAGAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
                                                                                                                                                                                  GGTTTTGGGGAAGGTATGTGCCGTCCAGGTGAAAAAACACTGGGAAGATGTATGCCTGTAAG
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                                                      GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
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                                                                                                                                                                GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG
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Pred. No. 6.3e-297;
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7; GRK7; cone visual signalling; visual sensitivity; visual resolution; night blindness; colour blindness; Oguchi disease; Fineal gland activit chronobiological desynchron; depression; anxiety; memory loss; headach mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
                                                                                                      Identifying compounds that alter inhibition of cone opsin kinase polypeptide activity for treating a conditions related to cone visual signaling, comprises mixing a compound with a cone opsin kinase and w an inhibitory polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2002; 2002WO-US007025
                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2001; 2001US-0274006P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cone opsin kinase (GRK7) OK6 splice variant cDNA
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/product= "Human GRK7
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Example

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Page 48-49;

61pp;

English

present

invention relates to novel

human

cone opsin

kinase

(G-protein

CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides. CC The invention further relates to a method of identifying compounds that CC alter the inhibition of GRK7 polypeptide activity which involves mixing a CC test compound with GRK7 protein and an inhibitory polypeptide and CC determining if the test compound alters the inhibition of GRK7 protein CC activity by the inhibitory polypeptide. GRK7 sequences are useful for CC treating conditions related to cone visual signalling (e.g., night CC blindness, colour blindness, difficulty with colour visual cC intensity, Oguchi disease or dominant congenital stationary night CC intensity, Oguchi disease or dominant congenital stationary night CC blindness), Pineal gland activity (e.g., chronobiological desynchrony, CC depression, anxiety, mental fogginess, memory loss, headaches, fatigue, CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide activity is beneficial, e.g., decreased colour sensitivity or orther cone photoreceptor mediated diseases. The GRK7 proteins are also useful in the CC probes to screen for inherited defects in colour vision, circadian rhythm CC and vision resolution. They are also used as gene therapy tools for CC spilce variant CDNA splice variant cDNA

Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;

DB 6; Length 1486;

В Ş 뮹 8 당 \$ В γQ 닭 8 Query Match Best Local Similarity Matches 1459; 831 481 421 711 361 301 601 891 541 771 651 591 241 531 181 471 121 411 351 291 61 GETTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCCATGGCTTTCTTGCAAGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACCTTCCACAGCCTGTGT 470 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACCAAGTGCCAAGCAGCCACCACTGAG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC GAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC GGGCTGCAGGGCTGCGCGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG Conservative 53.2%; ; Score 1170.4; ; Pred. No. 2.2e-0; Mismatches 2e-292; 6; Indels 275; Gaps 350 660 950 480 770 420 360 300 240 60

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226 GATAAGCATTCTTCAAAAACTTTGCGACGTGCTCTTCTTTTTTTT	₹ ₽
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— GAGAAAAGTICTGATGATTGATGCCAGGAAACATTTCTTTAAAACGATGATGTATATG CTGGAAGCATGCCTAATTGAACCCCCATTTTTTGCACACACA	Q F
611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 16	νQγ
1050 1049	Db
551	Qy
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491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCAC	Q
1050 1049	Db
1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490	Qy
1050 1049	В
1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTTGCCATGGGATGCAGC 1430	Qy
21 ATGAAGGCTGGCAAGCCCATCACCCAGAG104	DЬ
11 ATGAAGGGTTGGCAAGCCCATCACCCAGAGGGCTTGGAACCAATGGTTACATGG	γQ
1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310	B &
01 GCTGTGGGATGCTGCACTCCATGAACTCGGCATCGTCTATCGGGACATGAAG	Db
1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250	Qy
41 TACAACGTGGGCACGCGTGGACATGAGCCGGGTGATCTTTACTCGGCCCAGATA 90	Дb
31 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAC	β
B1 AAGACCCATCTCTCATCATCAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840	문
71 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGAAT	Q ·
721 GABATTTTGGGGAAAGGTCAGGAGCCCTTTCATTGTTTCTTTGAGCCCTTATGCTTTTTGAGAGC 78	B &
AAAG 720	\$ 8
51 AAACTGGACAAGAAGCGGCTGAAGAAAGAAAGATGGCTCTCTTGGAAAAG 10	\$ &

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                                                                       Matches 1048;
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                       screening libraries and assessing gene expression patterns. The nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRK expression. The nucleotides of the invention can be used to genetically engineer host cells to express GRK products in vivo. The nucleotide sequences of the invention are also useful in addressable arrays for identifying and characterising the temporal and tissue specific expression of a gene and in microarrays to screen collections of genetic material from patients who have a particular medical condition. The proteins of the invention are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to GRK, and as reagents in assays for screening for compounds that are useful in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NHP (novel human protein) in the specification, which is claimed in the invention. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-protein coupled receptor kinase; GRK; human; ss; gene therapy; drug screening; gene expression characterisation; NHP; novel human protein.
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                                                                                                                                                 Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 32; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotides of the invention are useful as hybridisation probes for
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                                                                                                                                                                       assays for screening to the confidence of medical disorders/diseases
                   291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG
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REFERENCE
AUTHORS
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Pred. No. the number of results predicted by chance to have

TITLE JOURNAL

Kapeller-Libermann,R. and Bandaru,R. Method and compositions of human proteins Patent: WO 02095032-A 1 28-NOV-2002;

and

uses thereof

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

Euteleostomi;

Homo.

KEYWORDS VERSION

Homo

sapiens sapiens

(human)

Sequence 1 AX797552 AX797552.1

GI:37518055

from Patent W002095032.

2198 bp

DNA

linear

PAT

04-OCT-2003

ALIGNMENTS

AX797552

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1657.2 1655.6 1655.6 1640.8 1422.2 1422.2 125 1187.8 1046.8 867.4 867.4 867.4 1988.8 1795.8 1757.8 1659.6 1658.4 1658.4 1658.7.2 419.8 418.8 418.2 418.2 418.2 418.2 411.2 419.6 409.6 586 572.4 553 425.6 424.6 1988.8 Score Query Match 100.0 91.4 90.5 1062 36651 36651 36651 36651 125041 215077 Length 2898 2105 2105 2105 2105 22632 2708 22848 22848 22549 22204 22204 22204 22448 22848 1761 1659 DB HUMPROCRKI AK056697 AF040749 AF040747 AR160365 U00686 I23378 I33280 AX329633 AB055658 AB009568 BOVRHKIN BC017272 AC068693 AC112504 AC068693 AF063016 BD186106 AR225818 AF282270 AY049726 AF040752 AF040751 AR343545 AX357904 AX252441 AR263767 AX710213 AX921933 AR343544 AX357902 AX252439 AR263766 AX642968 AR225817 AF439409 BD186115 AX797554 AX797552 AR225β19 AX252443 BC009277 IJ AX166511 U00686 Human putat 12378 Sequence 12 133280 Sequence 12 AX329633 Sequence L16862 Homo sapien AK056697 Homo sapi AF040749 Mus muscu AF040747 Mus muscu AF063016 Spermophil BD186106 A novel g AR225818 Sequence AX252441 Sequence AX252441 Sequence AX253767 Sequence AX357904 Sequence AX357904 Sequence AX068693 Homo sapi AC112504 Homo sapi AC068693 Homo sapi AC068693 Homo sapi AC07277 Homo sapi AF040751 Homo sapi AF040751 Homo sapi AF040751 Homo sapi AF040751 Homo sapi AX710213 Sequence AX921933 Sequence AF282270 Sus scrof AY049726 Bos tauru AF439409 Homo sapi BD186115 A novel g AX797554 Sequence AR343544 AX357902 AX166511 AR225817 Sequence AX252439 Sequence AR160365 Sequence AR263766 Sequence AX642968 Sequence Description Sequence Sequence Homo sapi Sequence Sequence

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475 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACCTTCCTAGCCACAGTGCCCACGTTCCGCA 534	355 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGGGGGGG	235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 294	Match 91.4%; Score 2008.8; DB 6; Length 2249; Local Similarity 99.9%; Pred. No. 0; Les 2010; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 175 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGAGGAAGCAG 234	ĕ	AR225819.1 GI:27263949 Unknown. Unknown. Unclassified. 1 (bases 1 to 2249) Walke, D.W., Wilganowski, N.L. and Turner, C.A. Human G-counted varietin recentor bisages, and	AR225819 2249 bp DNA linear PAT 20-DEC-2002 N Sequence 5 from patent US 6444456.	2161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTGA 2198	E 8=8 8=1
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355 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC	Qy 295 TGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 354 L	OY 235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 294	Dy 175 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 234	Query Match 91.4%; Score 2008.8; DB 6; Length 2249; Best Local Similarity 99.9%; Pred. No. 0; Matches 2010; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	SOUTCE 1249 /organism="Homo sapiens" /mol_type="unassigned DNA" /mol_type="taxon:9606" ORIGIN	Patent: WO 0 Lexicon Gene	REFERENCE 1 AUTHORS Walke, D.W., Wilganowski, N.L. and Turner, C.A. TITLE Human g-coupled protein receptor kinases and polynucleotides	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	LOCUS AX25443 DEFINITION Sequence 5 from Patent W00168869. ACCESSION AX252443 VERSION AX252443 GI:15985735	I 3	Qy 2155 TTTTCACTGAGGGAAAAGGAACACTCA 2186	QY 2095 CACTACTAGAACACATTTTATTTTCTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2154	QY 2035 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAACAA	OY 1975 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2034	QY 1915 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 1974	Qy 1855 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1914	OY 1795 AGCAGTTCTTCAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1854	DD 1798 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1857
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J. Neurosci. 21 (23), 9175-9184 (2001)
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                                                                                                       TCCCTGAACTTCCACAGCCTGTGTGAGCAGCCAGCCCATCGGTCGCCGCCCTCTTCCGTGAC
                                                                                                                               TCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGCTGGCCGCCTCTTCCGTGAC 506
                                                                                                                                                                                                            CGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTG
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HHFFKTINFPRLEAGLIEPPFVPDPSVVYAKDIAEIDDFSEVRGVEFDDKDKQFFKNF
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/protein_id="AAL33880.1"
/db_xref="GT:17026318"
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FEATURES source	1527 AAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCT 1586	₽ &
Bae Dir Sub Nor	1467 GATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTC 1526 	유 정
8888	1407 GACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAA 1466 	유 정
REFERENCE 1 (base AUTHORS Chen, C. X Chen, Y. J TITLE Characte	1347 ACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTG 1406 	유 성
SOURCE Homo sap ORGANISM Homo sap Eukaryot Mammalia	1287 TCTGACCTGGGGCTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGA 1346 	8
ACCESSION AF439409 VERSION AF439409	1227 GTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTA 1286	4d 4d
RESULT 6 AF439409 LOCUS AF439409 DEFINITION Homo san	1167 GTGATCTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATC 1226	용 성
	1107 GGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGG 1166 	8 8
Db 1921 TTCTTC Ov 2187 GGTTTA	1047 ICTCIGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAAT 1106	B &
Db 1861 ACAAAA Oy 2127 TTCTTC	GAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTC 840	문
рь 1801 тсттсс Оу 2067 асаааа	ACTEGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAGATGGC	문 :
2007	aggiggiiitigggaggiaigiigigccgic	& B
Qy 1947 TTGTAA Db 1741 TTGTAA	GAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAAC	Ϋ́
Db 1681 CCCAAC	807 GACAAGTITCTGCAGIGGAAACTCTTCGAGAIGCAACCAGIGTCAGACAAGTACTTCACI 866	유 성
1621	747 GAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTAC 806	dg Vy
Db 1561 CGGGGG		дЬ
Qy 1767 CGGGGG	*21 IGIG-GRAGCAGCCACCACTGAGGAAGAGAGCGAGTGGCTGGAGTGACTGCAGTGACGCTAAGACT 746	\$ 8
Qy 1707 CCAGAC	TGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCCTTCCTCAGCCAGGCCGTGGCCACC	\$ 8
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.K., Zhang,K., Church-Kopish,J., Huang,W., Zhang,H.,
.J., Frederick,J.M. and Baehr,W.
terization of human GRK7 as a potential cone opsin kinase is. 7, 305-313 (2001)
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Uphthalmology, University of Utah,
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Location/Qualifiers
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allele, complete cds.
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/mol_type="mRNA"
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/chromosome="3"
/map="3q21"
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,	Db Qy	Qy Db	Qy Db	Qy db	Db dy	Qy db	gg Qg	Qy Db	עס	D Qy	4g 4g	Db Qy		ORIGIN				gene
	814 TTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCA 873	754 TGGCTITCTTGCAAGAGCAGCCCTITAAGGATTTCGTGACCAGCGCCTTCTACGACAAGT 813	694 AAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCA 753	634 GTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCC 693	574 TGGCCGAGGAGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGA 633	514 CCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGC 573	454 ACTICCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAG 513	394 GTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGA 453	334 CCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGC 393	GCGCCCCGTGCTCAGCCATGGTGGACATGGGGGACAACCTGATCGCCAACACCG	214 TCACCCGGGAAGGGAAAGCAGCCAGCCGGCCTCCTGTGCTTTCCCTGGGAGT 273	154 ACCCTCCACGGGTCCCACACGACACGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTC 213	Query Match 81.7%; Score 1795.8; DB 9; Length 1799; Best Local Similarity 99.9%; Pred. No. 0; Matches 1797; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	DYKEKVSKEDLKQRTLQDEVKFQHDNFTEEAKDICRLFLAKKPEQRLGSREKSDDPRK HHFFKTINFPRLEAGLIESPFVPDESVVXAKDIAEIDDFSSVRGVEFDDKDKQFFKNF ATGAVPIAWQEEIIETGLFEELNDPNRPTGCEEGNSSKSGVCLLL"	QPFKDFVTSAFYDKFLQWKLFEMQPVSDKYFTEFRVLGKGGFGEVCAVQVKNTGKMYA CKKLDKKRLKKKGGEKMALLEKKYSSPFYSLAYAFESKTHLCLYMSLANGGDL KFHIYNVGTRGLDMSRVIFYSAQIAGGMLHAELGIVYRDMKPENVLLDDLGNCRLSD LGLAVENKGGKPITQRAGTNGYNAFELLMEKVYYSYPVDWFAMGCSIYEMVAGRTPFK	/db_xref="gI:17933259" //translation="mydmyaldnilantantayiqarkesdcdskelqrrrrslalpgiqg /translation="mydmyaldnilantayiqarkesdcdskelqrrrrslalpgiqg Caelrqkisinffisicorqpigfistatyptfrkaatfledvqnmelaaegftk DSALQGIVATCASAPAPGNPQPPISQAVATKCQAATTBEERVAAVTLAKAENVAFIQE DSALQGIVATCASAPAPGNPQPPISQAVATKCQAATTBEERVAAVTLAKAENVAFIQE		1e 11799 /gene="GRK7" /allele="S"
	D 43	B B	δ β <i>r</i>	0 P X) B &) Db Qy	A GA) B &	}	dg dg	D Qy	D DD VQ	Db Qy	dg Qy	Qy Db	Qy Db	ου	Qy Db
	ACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTT	TAGCATGCAGAAGAAATTATAGAAACGGGAACTGTTTGAGGAACTGAATGACCCCAACA		TTTGATGACAAAGATAAGCATTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTA	AAACG	CAGAGCAACGCTTAGGAAGCAAGAAAAATCTGATGATCCCAGGAAACATCATTTCTTTA	AGCATGATAACTTCACAGAGAAAGAAGATATTTGCAGGCTCTTCTTGGCTAAGAAAC	AUGARAAGSTCASTARANGAGATICTGAAGCARAAGAKITCTGCAAGAGAGAGAGAGAGATACA	TIGCCATIGGAATCCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACA	1354 GTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGT 1413	1294 TGGGGCTGGCGTGGAGATGAAGGGTGGCAAGGCCCATCACCCAGAGGGCTGGAACCAATG 1353	GGACATGAAGCCTGACAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACC	TTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATC	1114 ACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCT 1173	1054 CCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAG 1113	994 TGGCTCTCTTGGAAAAGGAAATCTTGGAGAAAGGTCAGCAGCCCTTTCATTGTCTCTCTGG 1053	934 AGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAAGGTGGCGAGAAGA 993 	874 GAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGA 933

Qy 746 TO	Qy 686 CAA Db 421 CAA	Qy 626 TI Db 361 TI	Qy 566 CI Db 301 CI	Qy 506 С! рь 241 С!	Qy 446 G] 	Qy 386 GCGG Db 121 GCGG	Оу 326 С! рь 61 С!	Qy 266 C1	Query Match Best Local Simi Matches 1759;	ORIGIN	FI FEATURES	م ت. در در د	PN P	4 . u ti ki	Mamm REFERENCE 1 AUTHORS Koya TITLE A no	WSI	2 <u>2</u>	RESULT 7 BD186115
AGGCCATGGCTTTCTTGC	AGTGCCAAGCAGCCACCA aGTGCCAAGCAGCCACCA	TTGTGCGAGTGCCCCTGCCC	3GGAGCTGGCCGAGGAGG 	CTTCCTAGCCACAGTGCCCA	CCTGAACTTCCACAGCC	3GCGGCGTAGCCTGGCCC 	CAACACGGCCTACCTGCAGG	GGAGTGCGCCCGTGCT	80.0%; larity 99.9%; Conservative (/organism="Homo sapiens /mol_type="genomic DNA" /db_xref="taxon:9606"	source 11761 /organism=' Location/Qualifiers 1 1761	NOBUYUKI KOYAMA, 63 C12N15/54, C12N9/1. novel gene relation coation/Onalifier	WO 02103020-A/10 27-DEC-2002 14-JUN-2002 WO 2002JP00594:	PATENT: WO 02103020-A 10 27 TAKEDA CHEMICAL INDUSTRIES YAMAMOTO	Sutheria; L to 1761) Tanida,S. ne relatir	2103020-A/10. sapiens (human) sapiens ryota; Metazoa;	yene relating .1 GI:3187831	
aagagcagccctttaaggi 	CTGAGGAAGAGCGAGTGG CTGAGGAAGAGCGAGTGG	CCGGGGAACCCGCAACCCT	GACCCACCAAAGACAGCG acccaccaaagacagcg	CGTTCCGCAAGGCGGCAA(CGTTCCGCAAGGCGGCAA(IGTGTGAGCAGCAGCCCAT	CGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGCAGAG	cccgaagccctcggact({	CAGCCATGGTGGACATGG CAGCCATGGTGGACATGG	Score 1757.8; DB 6 Pred. No. 0; D; Mismatches 2;	mo sapiens" nomic DNA" on:9606"	. 1761 organism='Homo sapiens ifiers	NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI YAMAMOTO C12N15/54, C12N9/12, G01N33/50, G01N33/15, C07K16, novel gene relating to disease and use thereof location/Onalifiers	02JP005942	RIES LTD, NOBUYUKI F	ini	data: Craniata:	1761 bp DNA disease and use	
TGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTA	CAAGTGCCAAGCAGCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGC	TTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAC 	CTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGGGGGCTGCAGGGGCTGGTGGCCAC 	CTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAA	GTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGA 	GCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAAGCTCCGCCAGAAGCT 	CAACACGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGCAACACACCGCCTACCTGCAGGCCGGAAGCCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGCAAAGAGCTGCAGCGCAAACACCTGCAAAGAGCTGCAGCGCAAACACCTACCGAACAGCAAAGAGCTGCAGCGCAAACAGCTGCAGCGCAAAGAGCTGCAGCG	CTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGC	; Length 1761; Indels 0; Gaps		ens (human)'.	YAMAMOTO 15,C07K16/40,A61K39/395 e thereof FH Key		7-DEC-2002; LTD,NOBUYUKI KOYAMA,SEIICHI TANIDA,KOJI	Hominidae thereof	Vertebrata: Euteleostomi	linear PAT 17-J thereof.	
TA 805	GC 745 	AC 685	AC 625	/AA 565 AA 300	'GA 505 GA 240	CT 445 	;cg 385 cg 120	;GC 325 	š 0;			/395 CC		A,KOJI		tomi:	17-JUN-2003	
DD 49	, B &	S B 7	S B 8	S B S	B &	£ £ \$	р ф	B &	S B 8	D 64	Qy Db	B Q	B 8	B &	Qy Db	Db Qy	Db Qy	Db
1826 TGTTCCTATAGCATGGCAGGAAGAAN	1 TCGGG	TCCAG	1381 TITUTIANAAACGATCAACTITCCTCC	TAAGA	1 CAAAI	AGATT	GGACT GGACT	AACC!	ATCTG	CGICI	1166 GGTGATCTTTTACTCGGCCCAGATAGG	1106 TGGGGGAGACCTCAAGTTCCACATCTF	1046 CTCTCTGGCCTATGCCTTTGAGAGCAA	986 CGAGAAGATGGCTCTCTTGGAAAAGGA 	926 CACTGGGAAGATGTATGCCTGTAAGAA 	866 TGAGTTCAGAGTGCTGGGGAAAGGTGG 	806 CGACAAGTTTCTGCAGTGGAAACTCTT	481 TGAGGCCATGGCTTTCTTGCAAGAGCA
CIRINGCATGGCAGGAAGAATTATAGAAACGGACTGTTTGAGGAACTGAATGA 1889 				AACCAGAGCAACGCTTAGGAAGCAGGAAAGTCTGATCATCCCAGGAAACATCA 1645 	TCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGC 1320	AL ARIOGANARIOGI CAGI RANIGANGAN IL IGANGCANAGANCI IC ICCANGCONGGI 1220	Tegritisca Teg	ATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGT 1140	ACCTGGGGCTGGACGTGAAGATGAAGGGTGGCAAGCCCAATCACCCAAGAGGCTGG	ATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTT 1285 	TCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCAT 1225	SAGACTICAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCG 1165	TGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAA 1105 	AGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGT 1045	SGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGA	TCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAA 925	AGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCAC 865	

Db 241 CGCAÁGGCGCAÁCCTTCCTÁGAGGCGAGACTGGCAGAGCTGGCCGAGGAGGAGGAGGACCC 300 Qy 591 ACCAAAGACAGCGCGCTGCAGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650		291 .1 351 61	/note="incyre in No: /4//204CB1" ORIGIN Query Match 75.5%; Score 1658.8; DB 6; Length 1662; Best Local Similarity 99.9%; Pred. No. 0; Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	ratent: wo ulubsa/-A 45 20-lik Incyte Genomics, Inc. (US) Location/Qualifiers 1. 1.662 1. 0.7ganism="Homo sapid" /mol_type="unassigned" /mol_type="taxon:96066" /mofe="Incyte In No.	Lal, P., Bandman, O. A.R., Tribouley, C. Id, S.R., Ramkumar, D.B., Tang, Y.T., B D.B., Tang, Y.T., B D.B., A., Patterson, C., S.A., Azimzai, Y., V.S., Thangavelu, Kinases	AX642968.1 GI:28550117 Homo sapiens (human) M Homo sapiens (human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ev Mammalia; Eutheria; Primates; Catarrhini; Hominidae; i	RESULT 9 AX642968 AX642968 AX642968 AX642968 DIA linear PAT 24-FEB-2003 DEFINITION Sequence 45 from Patent WO01096547. ACCESSION AX642968	Qy 1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTATTG 1949	Db 1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
1671 CGCCI 1381 CGCCI 1731 AAAGI 1741 AAAGI 1791 GATAA 1501 GATAA	Db 1201 GAGGATCTGAAGGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260 Qy 1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTGGCTAAGAAACCAGAGCATGATAAGA 1610		1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG	Qy 1191 GCCTGTGGGATGCTGCACGTCCATGAACTCGGCATCGACGACATGAAGCCTGAG 1250	OY 1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAGTGGGGAGACCTCAAGTTCCACATC 1130	OY 951 AAACTGGACAAGAAGCGGCTGAAGAAGGAAGAAGGTGGCGAGAAGATGGCTCTCTTTGGAAAAG 1010	891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 	Db 481 CAGCCCTTTÀAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAAGTC 540 Qy 831 TTCGAGATGCAACCAGTGCAGACAAGTACTTCACTGAGTTCAGAGTGCGGGAAAGGT 890	QY 771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830

, DB QV DB QV QV QV	0y .	D Q D Q	Db Db	& & &	ORIGIN Query Match Best Local : Matches 165:	TITLE JOURNAL FEATURES source	SOURCE ORGANISM REFERENCE AUTHORS	RESULT 10 AR225817 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy db	Qγ Db
711 GAAGAGCGAGTGACGTGACGCTGCGCAAGGCTGAGGCTATGCTTGCAAGAG 770	591 ACCAAAGACAGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650	471 GAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530	61 AAGCCTTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCC 120 411 GGGCTGCAGGGCTGCGCGGACGCCAGAAGCTGCCCTGAACTTCCACAGCCTGTGT 470	TGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 35	Similari	Human G-coupled protein receptor kinases and encoding the same L Patent: US 6444456-A 1 03-SEP-2002; Location/Qualifiers 1. 1662 /organism="unknown"	Uhknown. SM Unknown. Unclassified. E 1 (bases 1 to 1662) E Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.	N O	1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952 	1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
5	2 P P P	0	S B & B	7 Q Db Q	Db Db	Qy Db Qy	D Qy	24 A2 A2	D Q (P 89
191 GATAGCAGTICTICAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGCAGGAAAAAACTTTGCGACAGGTGCTGTCCTATAGCATGCAGGAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGCAGGAAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAAAAAACTTTGCGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910	CATE A COLOR TENTED A A A TENTE COLOR TENTE COLOR TENTE CALADA	1511 GROCAGGARAGATATITICABACCTCTATTTCTTTAAAACGATCAGGCTTAGGA 1320 1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACCTTTCCT 1670 1611 AGCAGAGAAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAAAACGATCAACTTTCCT 1670 1321 AGCAGAGAAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380 1521 AGCAGAGAAAAGTCTGATGATCCCAAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380	ATTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA GAGGATCTGAAGCAAAGAACTCTGCAAGACGACGACGTCAAATTCCAGCATGATAACTTCACA	ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC	961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020 1311 ATGAAGGGTGGCAAGCCCAATCACCCAGAGGGCTGGACCCAATGGTTACATGGCTCCTGAG 1370	1191 GCCTGTGGGATGCTGCACCTCCATGAACTCCGCCATCGTCTATCCGGACATGAAGCCTGAG 1250	TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA	1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTGTGGGCTATGCCTTTGAGAGC 1070	AAACTGGACAAGAAGCGGCTGAAGAAGAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG	891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950

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991 GGTTTTGGGGAAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950	31 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890	771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830	711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770	651 AACCCGCAACCCTTCCTCAGCCAGGCGGGGCACCACGAGTGCCAAGCAGCCACCACTGAG 710	591 ACCAAAGACAGOGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650	531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGAGGACCC 590	471 GAGCAGCAGCCGATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGCTTC 530	411 GGGCTGCAGGGCTGCGCGGAAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470	51 AAGCCCTGGGACTGCGACAGCAAAGAGCTGCAGCGGCGGGGGGGG	91 ATGGTGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350	ch 75.5%; Score 1658.4; DB 6; Length 1662; Similarity 99.8%; Pred. No. 0; Sonservative 1; Mismatches 2; Indels 0; Gaps 0;	AX252439 AX252439 AX252439 AX252439 AX252439.1 GI:15985733 . Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Craniate; Catarrhini; Hominidae; Homo. 1 Malke, D.W., Wilganowski, N.L. and Turner, C.A. Human g-coupled protein receptor kinases and polynucleotides encoding the same Patent: WO 0168869-A 1 20-SEP-2001; Lexicon Genetics Incorporated (US) Location/Qualifiers 1. 1662 /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"

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1 (Dases 1 to 1662)

Guegler,K., Beasley,E.M. and Di Francesco,V.
Isolated human kinase proteins, nucleic acid
human kinase proteins, and uses thereof
Patent: US 6331423-A 1 18-DEC-2001;
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Similarity 99.8%;
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   GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
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Sequence 1 from AR343544 AR343544.1 AR343544

patent

1662 bp : US 6579709.

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PAT 17-AUG-2003

Unknown. Unknown.

GI:33739257

AUTHORS Unclassified.
1 (bases 1 to 1662)
Guegler, K., Beasley, E.M. and Di Francesco, V.

B	FEATURES SOURCE ORIGIN Query Mat Best Loca Matches 1 Qy 2 Qy 3 Qy 4 Qy 4 Qy 4 Qy 4 Qy 4 Qy 5 Db 1 Qy 5 Db 1 Qy 6 Qy 6 Qy 6 Qy 7 Qy 7 Db 3 Qy 8 Qy 8 Qy 9 5 Db 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	TITLE
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RESULT 14 AX357902 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM FEFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	B	Qy
AX357902 AX357902 N Sequence 1 from Patent WOO192496. N AX357902 N AX357902.1 GI:18674690 Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. E 1 Guegler, K., di Francesco, V. and Beasley, E.M. Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof Patent: WO 0192496-A 1 06-DEC-2001; Applera Corporation Robert A. Millman Assistant Secretary (US) Lostion/Qualifiers 1. 1662 /organism="Homo sapiens"	901 GCCTETGGAGATGCTCCCCCCCCCCCCCCCCCCCCCCCCC	1191 GCCTGTGGGATGGTCTATCGGC

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Sequence 2 from Patent W00138503.
AX166511
                                                                                                                                        Flanagan, P. and Clary, D.S.

Novel human protein kinases and protein Patent: WO 0138503-A 2 31-MAY-2001;
                                                                                                                                                                                        Plowman, G.D., Whyte, D., Manning, G.S.,
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DN
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                                                                                                            Location/Qualifiers
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 75.3%;
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1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250	Ş.
841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900	Db
1131 TACAACGIGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190	γQ
781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840	dd
1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC 1130	Q.
GAAATCTTGGAGAAGGTCAGCACCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAG	Db
1011 GAAATOTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070	Qγ
661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAA 720	ф
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891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAAACACTGGGAAGATGTATGCCTGTAAG 950	Ş
541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600	Вb
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481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540	DЪ
771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830	8
421 GAAGAGCGAGTGGCTGGAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480	뭉
711 GAAGAGCGAGTGACTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCCTTGCAAGAG 770	γQ
361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420	문
651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAAGTGCCAAGTGCCAGCCA	Ş
301 ACCAAAGACAGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCCGGG 360	Db
591 ACCAAAGACAGCGCCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650	Qy
241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300	하
531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590	γQ
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121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCCTGAACTTCCACAGCCTGTGT 180	Db
411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470	8
61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC	당 .
351 AAGGCCTTGGGACGACGAGAGAGAGCTGCAGGGGGGGGGG	₹
ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCCCCTACCTGCAGGCCCGG 60	당 성
Best Local Similarity 99.8%; Pred. No. 0; Matches 1658; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Best Matcl

Qy Db	Qy Db	Qy Db	Qy db	QQ dd	Qy Db	Qу Db	Qy Db	A5 40	B &	Db
1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA	1851 ATTATAGANACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 	1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 	1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA	1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC	1611 AGCAGAGAAAAGTCTGATGATGCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT	1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 	1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 	1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAAGGTCAGTAAA	1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC	1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG
A 1952 A 1662	CAGACCTACGGGTTGTGAG 1910	CATAGCATGGCAGGAAGAA 1850 RTAGCATGGCAGGAAGAA 1560	EGTGGAATTTGATGACAAA 1790 EGTGGAATTTGATGACAAA 1500	CCTTCAGTGGTTTATGCC 1730	PAAAACGATCAACTTTCCT 1670	CCAGAGCAACGCTTAGGA 1610		DAGGAAAAGGTCAGTAAA 1490 TAGGAAAAGGTCAGTAAA 1200	TTTGCCATGGGATGCAGC 1430	GGTTACATGGCTCCTGAG 1080

Search completed: August 13, 2004, 16:48:46 Job time : 5731.66 secs

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17 US-10-451-168-49
15 US-10-217-745-5
15 US-10-217-745-1
9 US-09-964-469-1
15 US-10-425-962-1
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Sequence 3, Appli
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e 1539	US-10-152-319A-			132.4	8
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Sequence 23. Appl	US-10-087-684-2	037 13	Ļ	151	3
Sequence 25, Appl	US-091771-161A-25	679 9	Ļ	151	30
Sequence 45. Appl	US-09-955-999-45		9.2 3	153.4	29
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Sequence 1. Appli	5 US-10-325-430-1	2113 15	19.3 2	320.6	27
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION UNMBER: US 60/241,884
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,877
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KAPELLER-LIBERMANN, Rosana
APPLICANT: BANDARU, Rajasekhar
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Proteir
TITLE OF INVENTION: Uses Thereof
TILE REFERENCE: 10147-5201
CURRENT APPLICATION NUMBER: US/10/044,205A
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                               61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGGCGTAGCCTGGCCCTGCCC
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AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACGAGTGCCAAGCAGCAGCACCACTGAGACCACCAAGCCACCAAGCCACCAAGCCACCAAGCCACCA
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AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG

ERAL INFORMATION:

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APPLICANT: KAPELIER LIBERMANN, ROSANA
APPLICANT: BANDARU, Rajasekhar
TITILE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Proteir
TITILE OF INVENTION: Uses Thereof
FILE REFERENCE: 10147-52U1
CURRENT APPLICATION NUMBER: US/10/044,205A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SECTIMARE: Patentin version 3.1 100.0%; Score 1659; sery Match 100.0%; Pred. No. 0; ocal Similarity 100.0%; Pred. No. 0; tches 1659; Conservative 0; Mismatches Q ID NO 1 LENGTH: 2198 0-044-205A-1)RGANISM: Homo sapiens DB 14; Length 2198;

351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCCTGGCCC

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180 410 291

181 GAGCAGGAGCCCATCGGGAGCTCCCGCCAGAAGCTGTCCCTGAACCTTCCACAGCCCTGTGT 470 181 GAGCAGGAGCCCATCGGTGGCCGGCTCTTCCGTGACCTTACCCACAGCCTAGCCCACGTTC 240 471 GAGCAGCAGCCCATCGGTGGCCGCCTCTTCCGTGACCTACCCACGTTCCCACGTTC 240 471 GAGCAGCAGCCCATCGGTGGCCGCCCTCTTCCGTGACCTACCCACGTGCCCACGTTCC 300 241 CGCAAGGCGGCAACCTTCCTCAAGAACACGTGCCCACGTGGCCCACGTGCCCAGGGGACCC 531 CGCAAGACAACGCGCTGCCAACGTGCCAAGACTTGGCAAGTGGCCCACGTGGCCCAGGGGACCC 531 ACCAAAGACAGCGCCTTCCTCAAGGAGCTGGCCAACTTGGCCAAGTGGCCCACGCCGCGGGGGACCC 531 ACCAAAGACAGCGCCTTCCTCAAGGAGCTGGCCAACTTGTGCCAAGTGCCCCCGCCCCGGGGGGACCC 531 ACCAAAGACAGCGCCTTCCTCAAGGAGCTGGCCAACTTGTGCCCAAGTGCCCCCCGCCCCCGGGGGGACCC 531 ACCCAAAGACCCATTCCTCAAGCAGGCCTTGGCCAACTTGTGCCCAAGTGCCCACCCCTAGG 541 AACCCCGCAACCCTTCCTCAAGCAGGCCTTGCCCAAGGTGCCAACTTTCTTGCAAGAACTC 542 GAAGACCGATTGCTCAACAATGACCCTTCCTCAAGCACACCAAGTTCCTTCC	411 GAGCTIGCAGGGCTGCGCGGAGAGCTCTCCAGAAGCTGTCCACAGCCCTGTTACTAGCACAGCCTTTTCCACAGCCCTGTTTCCACAGCCCTGTTTCCACAGCCCTGTTTCCACAGCCCTGTTTCCACAGCCCTGTTTCCACAGCCCACAGTTTCCACAGCCCACAGTTTCCACAGCCCACAGTTTCCACAGCCCACAGTTTCCACAGCCCACAGTTTCCACAGCCCACAGTTTCCACAGCCCACAGTTCCACAGCCCACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACAGTTCCACACAGTTCCACACAGTTCCACACAGTTCCACAGCCCACAGTTCCACAGCCCACACCCACC
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RESULT 3
US-10-311-034-45

VS-Quence 45, Application US/10311034
Publication No. US20040023242A1

Publication No. US20040023242A1

Publicant: INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: AU-YOUNG, Janice
APPLICANT: AU-YOUNG, Janice
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TAO, Monique G.
APPLICANT: VAO, Monique G.
APPLICANT: GREENWALD, Sara R.
APPLICANT: HAFALIA, Jamiel B.
APPLICANT: HAFALIA, April
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APPLICANT: HAFALIA, April
APPLICANT: MONTON, Michael
APPLICANT: MONTON, Michael
APPLICANT: MONTON, Shirley A.
APPLICANT: AZINZAI, Yalda
APPLICANT: AZINZAI, Yalda
APPLICANT: GRETHER, Megan
APPLICANT: BAIRA, Sajeeev
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SOFTWARE: PERL I
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LENGTH: 1662
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
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OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
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                                              AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAAG
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Pred. No. 0;
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RESULT 4
US-10-451-168-49
Sequence 49, Application US/10451168
; Sequence 49, US20040091969A1
; Publication No. US20040091969A1
; GENERAL INFORMATION: APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. APPLICANT: GLAXO GROUP LIMITED TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GP5003 CURRENT APPLICATION NUMBER: US/10/451,168 CURRENT FILING DATE: 2003-11-12

Oy 601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAACACTGGGAAGATGTATGCCTGTAAG 660	QY 541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600	QY 481 CAGCCCTTTAAGGATTTCGTGAGCCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540	Qy 421 GAAGAGCGAGTGGCTGCAGTGACGCCTGCGCAAGGCCTGAGGCCATGGCTTTCTTGCAAGAG 480	Qy 361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420	Qy 301 ACCAAAGACAGCGCGCTGCAGGGGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360	Qy 241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTTGGGAGGTGGCGAGGAGGACGGAC	Qy 181 GAGCAGCACCATCGGTCGCCGCCTCTTCCGTGACCTTCCTAGCCACAGTGCCCACGTTC 240	Qy 121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAACCTGTCCCTGAACTTCCACAGCCTGTGT 180	Qy 61 AAGCCCTCGGACTGCGACAGCAAGAGCTGCAGCGGGGGGGG	Qy 1 AIGGTGGACATGGGGGCCCTGGACAACCTGATCGCCTACCTGCTGCAGGCCCGG 60	Query Match 99.8%; Score 1655.8; DB 17; Length 1662; Best Local Similarity 99.9%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	; TYPE: DNA ; ORGANISM: Homo sapiens US-10-451-168-49	; NUMBER OF SEQ ID NOS: 110 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 49 ; LENGTH: 1662	FILING DATE: 2001-04-04 APPLICATION NUMBER: 60/289, FILING DATE: 2002-06-28	; PRIOR ETLING DATE: 2001-01-30; PRIOR APPLICATION NUMBER: 60/266,797; PRIOR FILING DATE: 2001-02-06	; PRIOR APPLICATION NUMBER: 60/260,482 ; PRIOR FILING DATE: 2001-01-09 ; PRIOR APPLICATION NUMBER: 60/264,922	; PRIOR FILING DATE: 2000-12-19 ; PRIOR APPLICATION NUMBER: 60/257,048 ; PRIOR FILING DATE: 2000-12-20	PRIOR APPLICATION NUMBER: PCT/US01/49232 PRIOR FILING DATE: 2000-12-17 PRIOR APPLICATION NUMBER: 60/256,710
RESULT 5 US-10-217-745-5 ; Sequence 5, Application US/10217745	QY 1621 GAGGGTAATTCAICCAAGTCTGGCGTGTGTTTGTTATTG 1659	QY 1561 AITATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	QY 1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	QY 1441 AAAGACATCGCTGAAATTGATGATTATTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500	QY 1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440	QY 1321 AGCAGAGAAAAGTCTGATGATCGCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380	QY 1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320	Qy 1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGGATGATAACTTCACA 1260	Qy 1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200	Qy 1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140		Qy 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020	OY 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960	841 TACI	ω,	QY 721 GAAATCTTGGAGAAAGGTCAGCAGCCCTTTCATTGTCTCTCGGCCTATGCCTTTGAGAGC 780	661	

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; Publication No. US20030004328A1
; GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
ITITLE OF INVENTION: No. US20030004328A1el Hu
ITITLE OF INVENTION: Encoding the Same
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ITILE OF INVENTION: USA001010 NUMBER: US/10/217,745
CURRENT APPLICATION NUMBER: US/09/802,117
PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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GAGGGTAATTCATCCAAGICTGGCGIGIGITTGTTATIG 1659
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Sequence 1, Application US/10217745
Publication No. US20030004328A1
GENERAL INFORMATION: APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.

Qy 601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAACACTGGGAAGATGTATGCCTGTAAG 660	5 481 5 41 5 41	361 361 421 421	241 241 301 301	Db 181 GAGCAGCAGCCATCGGCCGCCAGCATTCCTCAGCCACAGTCCACAGCTTC 240 Db 181 GAGCAGCAGCCCATCGGTCGCCGCCAGAAGCTTCCTAACTTCCACAGCCTGTT 240 Db 181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240 Db 181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240	. 61 1	Query Match Best Local s Matches 1656	OF INVENTION: Polynucleotides OF INVENTION: Encoding the Same REFERENCE: LEX-0147-USA IT APPLICATION NUMBER: US/10/217,745 IT FILING DATE: 2002-08-12 APPLICATION NUMBER: US/09/802,117 FILING DATE: 2001-03-08 I OF SEQ ID NOS: 5 RE: FastSEQ for Windows Version 4.0 NO 1 DNA NO 1 H: 1662 DNA ISM: homo sapiens	030004328Alel Human G-Coupled Protein Recentor Vincon
RESULT 7 US-09-964-469-1 i Sequence 1, Application US/09964469 i Petent No. US20020034803A1 i GENERAL INFORMATION: i APPLICANT: GUEGLER, Karl et all i TITLE OF INVENTION: ISOLATE HUMAN KINASE PROTEINS, NUCLEIC ITITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES ITITLE OF INVENTION: THEREOF ITITLE OF INVENTION: THEREOF ITITLE OF INVENTION: UNMEER: US/09/964,469 CURRENT APPLICATION NUMBER: US/09/964,469 CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 60/208,331	Db 151 GAGGGTAATTCATCCAAGTCTGGGGTGTGTTGTTTGTTATTG 1659 1621 GAGGGTAATTCATCCAAGTCTGGGGTGTGTTTGTTATTG 1659	1441 1441 1501 1501	1321 AGCACA 1321 AGCACA 1321 AGCACA 1381 CGCCTG 1381 CGCCTG	1201 GAGGAT 1201 GAGGAT 1261 GAGGAA 1261 GAGGAA 1261 GAGGAA	1081 ATCCTS 1081 ATCCTS 1081 ATCTTAN 1141 ATTTAN 1141 ATTTAN 1141 ATTTAN	1021 1021	Db 781 AAGACCCATCTCTGCCTTGTCATGAACTCGGCATGATGTGACCTGAAGTTCCAAGTA 2y 841 TACAACGTGGGCACGCGTGGCCTGGACATGAGGCGGGTGATCTTTACTCGGCCCAGATA 20 841 TACAACGTGGGCACGCGTGGCCTGGACATGAGGCGGGTGATCTTTTACTCGGCCCAGATA 20 841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 20 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATACCTGAAGCCTGAG 2y 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 20 901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 20 901 GCCTGTGGGATGCTTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 20 901 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTTGGGGCTGGACGTTGAC 20 961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTTGGGGCTGGACGTTGACCTTGAACTTGAACTTGGAGGTTATCTGACTTGGGGCTTGACCTTGAACTT	

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Best Local
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PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
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ORGANISM: Human
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                                        AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
AAGACCCATCTTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC 840
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1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGGTGGAATTTGATGACAAA 1500	Qy
1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440	рь
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1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080	80
961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTIGGCCGTGGAG 1020	Db
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901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960	Ş
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RESULT 8
US-10-425-962-1
US-10-425-962-1
; Sequence 1, Application US/10425962
; Sequence 1, Decided on US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION: US20030180786A1
; GENERAL INFORMATION: ACID HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV2
; CURRENT APPLICATION NUMBER: US/10/425,962
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/564,469
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR PILING DATE: 2000-128
; PRIOR FILING DATE: 2000-106-01
; PRIOR FILING DATE: 2000-06-01

AND USES

Oy 601 GSTTTTGGGGAGGTATGTGCCTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660 Db 601 GSTTTTGGGGAGGTATGTGCCTCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660 GSTTTTGGGGAGGTATGTGCCTCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660 Qy 661 AAACTGGACAAGAAGCGGCTGAAGAAGATGGTGGCGAAAAAGTGGCTCTTTGGAAAAG 720 Db 661 AAACTGGACAAGAAGCGGCTGAAGAAAAGGTGGCGAAGAATGGCTCTTTGGAAAAG 720 Qy 721 GAAATCTTGGAGAAGGTCAGCCCTTTCATTGTCTCTCTGGCCTTTGAGAGC 780	361 421 421 481 481 541		NUMBER OF SEQ ID NOS: 4
RESULT 9 1 Sequence 273, Application US/10072012 1 Publication No. US20040033493A1 2 FUDLICANT: Tchernev, Velizar APPLICANT: Spytek, Kimberly APPLICANT: Zerhusen, Bryan APPLICANT: Patturajan, Meera APPLICANT: Li, Li APPLICANT: Li, Li APPLICANT: Padigaru, Muralidhara APPLICANT: Anderson, David W. APPLICANT: Anderson, David W. APPLICANT: Maller; Charles E. APPLICANT: Miller; Charles E. APPLICANT: Gerlach, Valerie APPLICANT: Gusev, Vladimir Y. APPLICANT: Gusev, Vladimir Y. APPLICANT: Gusev, Vladimir S. APPLICANT: Colman, Steven D. APPLICANT: Gusev, Vladimir S. APPLICANT: Gusev, Vladimir Y.	OY 141 AAAGACATCGCTGAAATTGATGATTATCTCTGAGGTTGGAGTTGATGACAAA 1500	1201 GAGGATCTGAAGAAGAAGTCTTGCAAGAAGAGAGGTCAAATTCCAGCATGATAACTTCACA	Db 901 GCCTGTGGGATGCTCCATGAACTCCGGCATCGTCTATCGGGACATGAAGCCTGAG 960 Qy 961 AATGTGCTTCTGGATGACCTCCATGAACTCGGGATCGTCTATCGGGACATGAAGCCTGAG 1020 p61 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGAGCTGAG 1020 p61 AATGTGCTTCTGGATGACCTCCGCAACTGCAGGTTATCTGACCTGGGCTGGCCGTGAG 1020 Qy 1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080 pb 1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080 Qy 1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGCATGCAGTCAGC 1140 pb 1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140 Qy 1141 ATTTATGGAAATGGTAGGTAAGTTATTCCTATCCTGTGGACTGAGAAAAGGTCAGTAAA 1200 pb 1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGGTAAAGGGTCAGTAAA 1200 1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGGTAAAGGGTCAGTAAA 1200 1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGGTAAAGGGTCAGTAAA 1200

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; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
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APPLICANT: Rieger, Daniel K.
APPLICANT: Buzgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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SOFTWARE: PatentIn Ver. 2.1
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APPLICATION NUMBER: 60/266,767
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                 GACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAG 1554
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APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an TITLE OF INVENTION: Encoding the Same
FILE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/10/217,745
CURRENT APPLICATION NUMBER: US/09/802,117
PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
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LENGTH: 1062
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Publication No. US20030004328A1
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ORGANISM: homo sapiens
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                                                                                              GAAGAGCGAGTGGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG
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Patent No. US20020034803A1
                                                                                                                                                                                                                                                                                                               LENGTH: 36651
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or G
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Similarity 96.8%;
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    Mismatches

                                                                                                      Score 617.4; DB 9;
Pred. No. 1.5e-178;
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; NAME/KEY: misc_feature
; LOCATION: (1) ... (36651)
; OTHER INFORMATION: n = A,T,C or
US-10-425-962-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10425962 Publication No. US20030180786A1 GENERAL INFORMATION:
                                                                                                                                                         SEQ ID NO 3
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/425,962
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: 09/964,469
PRIOR FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUEGLER, KAYL et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOGSSCIVE TO ACC ACC ACC
                                                                                                                                                                       PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/208,331
                                                                                               ORGANISM: Homo sapiens
                                                                               FEATURE:
                                                                                                                                       ENGTH: 36651
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                    GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 651
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APPLICANT: Benovic, Jeffrey L.
APPLICANT: Gomez, Jorge
APPLICANT: Gomez, Jorge
APPLICANT: Kunapuli, Priya
ITITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G Protein-
ITITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G Protein-
ITITLE OF INVENTION: Receptor Kinases GRK5 and GRK6
ITITLE OF INVENTION: Receptor Kinases GRK5 and GRK6
ITITLE OF INVENTION IN INTELLIBENCY
CURRENT FILING DATE: 2001-10-01
CURRENT FILING DATE: 2001-10-01
CURRENT FILING DATE: 2001-10-01
FRIOR APPLICATION NUMBER: US 08/464,954
PRIOR APPLICATION UNMBER: US 08/464,954
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION UNMBER: US 08/076,084
PRIOR FILING DATE: 1995-06-11
VUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 2848
TYPE: DNA
ORGANISM: Homo sapiens
US-09-851-686-2
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RESULT 13 US-09-851-686-2

Sequence 2, Application US/09851686
Patent No. US20020034767A1
GENERAL INFORMATION:

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Query Match
Best Local Similarity
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         GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG
                                                    GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
                                                                                                                               GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018
                                                                                                                                                                                   GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT
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Pred. No. 1.1e-117;
0; Mismatches 683;
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                                                                                 APPLICANI: DAUGE, NOTHING PRIOR PELLON NUMBER: US/09/873,367C
CURRENT APPLICATION Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-19-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
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STATE PATENT DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: PATENTIN VETSION 3.0
TENTYPH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-142
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US-09-873-367C-142
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Publication No. US20
GENERAL INFORMATION:
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APPLICANT:
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Publication No. US20030228689A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 890; Conserv
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CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
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TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
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                              125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184
                                                                                                                                                                                                                                             15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG
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GGTTACATGGCTCCTGAGATCCTAATGGA 1091 	
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CGGGACATGAAGCCTGAGAATGTGCTTCT 971 	912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT
TITTACTCGGCCCAGATAGCCTGTGGGAT 911	852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT
GACCTCAAGTTCCACATCTACAACGTGGG 851 	792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCGACATCTACAACGTGGG
SSCCTATGCCTTTGAGAGCAAGACCCATCT 791	732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT
ATGGCTCTTGGAAAGGAAATCTTGGA 731 	672 GAAGCGGCTGAAGAAGAAGATGGCGAGAAGATGGCTCTTTGGAAAAGGAAATCTTGGA
BAGATGTATGCCTGTAAGAAACTGGACAA 671 BAGATGTATGCCTGCAAGAAGCTAGAGAA 718	612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA
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GAGTGCCCCTGCCCCGGGGAACCCGCAACC 371	65
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Search completed: August 13, 2004, 19:06:12 Job time : 527.034 secs Jam K- Sheet

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GenCore version 5.1.6
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Search time 4319.34 Seconds (without alignments) 16647.489 Million cell updates/secctggcgtgtgtttgttattg 1659 residues nmeters: 6940544
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS	ID AX797554 AX797552 AX642968 BD186115 AF8439409 AR225813 AX710216 AF282269 AR225837 AR245343 AX710216 AF282269 AR255817 AX357902 AX166511 AX710213 AX7043726 AF043726 AF043757 AF040751 AF040749	SUMMARIES
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AUTHORS TITLE JOURNAL	REFERENCE	SOURCE ORGANISM	RESULT 1 AX797554 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS
Kapeller-Libermann,R. and Bandaru,R. Method and compositions of human proteins and uses thereof Patent: WO 02095032-A 3 28-NOV-2002;	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1	Homo sapiens (human) Homo sapiens	AX797554 1659 bp DNA linear PAT 04-OCT-2003 Sequence 3 from Patent WO02095032. AX797554 AX797554.1 GI:37518056

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                                                                             TACAACGTGGGCACGCGTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
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DEFINITION ACCESSION VERSION RESULT 2 AX797552 LOCUS SOURCE ORGANISM KEYWORDS REFERENCE FEATURES AUTHORS TITLE JOURNAL source Sequence 1 from Patent W002095032. AX797552 AX797552.1 GI:37518055 Kapeller-Libermann,R. and Bandaru,R. Method and compositions of human proteins Patent: WO 02095032-A 1 28-NOV-2002; MILLENIUM PHARMACEUTICALS, INC. (US) Homo sapiens Homo sapiens (human) AX797552 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo. /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" Location/Qualifiers and uses

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                                AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGGCTGGCCGTTGGAG
                                                                                                      GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG
                                                                                                                                                      TACAACGTGGGCACGCGTGGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA
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                                                                                       Patent: WO 01096547-A 45 20-DEC-2001; Incyte Genomics, Inc. (US)
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases I to 1761)

Koyama, N., Tanida, S. and Yamamoto, K.
Koyama, Parent; WO 02103020-A 10 27-DEC-2002;

PAKEDA CHEMICAL INDUSTRIES LTD, NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI
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                                                 14-JUN-2002 WO 2002JP005942
15-JUN-2001 JP 01P 182654
NOBUTUKI KOYAMA, SEIICHI TANIDA, KOJI YAMAMOTO
C12N15/54,C12N9/12,G01N33/50,G01N33/15,C07K16/40,A61K39/395
novel gene relating to disease and use thereof FH Key
Location/Qualifiers
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WO 02103020-A/10
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Direct Submission
Submitted (23-OCT-2001) Ophthalmology, University of Utah,
Submitted (23-OCT-2001) Take City, UT 84112, USA
North/2030 East, Salt Lake City, UT 84112, USA
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SOURCE ORGANISM Homo sapiens sapiens (human)

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                                                                       GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCCTTTGAGAGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases I to 3186)
Weiss, E.R., Ducceschi, M.H., Horner, T.J., Li, A., Craft, C.M. and Osawa, S.
                                                                                Homo sapiens
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421 GAAGAGCGAGTGGCTGCACAGGCGAGGCGTTGCTTGCAAGAGCGGGGGGGG			241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGAG	181 GAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCCACGTTC 240			ATGGTGGACATGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG	1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 1 ATGGTGGACATGGGCAACGTGATGGCCAACACGGCCTACCTGCAGGCCCGG 60	99.8%; Score 1655.8; DB 9; Length 3186; Similarity 99.9%; Pred. No. 0;	LGLAVEMAGGER I I VERGE INGERERE ELIMEN OF DE ER PER FERENCE DE REKSDDPRK DYKEKVESKEDLKORTLODEVKEODINEFTEEAKD I CRLEFLAKKEORGUEEDDKOKOFFKNF HHFFKTINFPRLEAGLI BPPFVPDPSVVYAKDI ABI DDFSEVRGVEEDDKOKOFFKNF ATGAVP I AWQEEI I ETGLFEELNDPNRFTGCEEGNSSKSGVCLLL"	DSALOGLVATCASABAPCKPOPTEISQAVATICOQAATIEBEK VAAVILAKAAAVAT LUG OPFKDFVTSAFYDKFLOMKLFEMGPVEDKYETEERVLGKGFGFEVCVAVQVKAVIGKNYA CKKLDKKRLKKKGGERVAALLEKEILEKVSSFFIVSLAVAFESKTHLCLVMSLANGGDL CKKLDKKRLKKKGGERVAALLEKEILEKVSSFFIVEDDERAMGGATVENVAGETEK KFHIYNVGTRGLDMSRVIFYSAQIACGUNEKVSVFNTDERAMGGATVENVAGETEK	/protein_id="AAI33880.1" /protein_id="AAI33880.1" /db xref="GI:17026318" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSKELQRRRRSLALPGLQG" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSkellqq" //tainslation="MYDMQALDNILIANTAYLQARKPSDCDSkellqq" //tainslation="MYDMqald" //	85. 1746 /note="protein kinase; GRK7" /codon_start=1 /product="G_protein-coupled_receptor_kinase_7"	/mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="retina"		Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA	s 1 to 3186) and Weiss, E.R. ubmission	Cells: implications for come cell provoctamenuction J. Neurosci. 21 (23), 9175-9184 (2001) 21574315 11717351	Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian come photoreceptor
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1585 GATAAGCACTTCTCAAAAACTTTCCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1644 1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGAGCCCAACAGACCTACGGGTTGTGAG 1620 	1525 AAAGACATCGTTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1584 1501 GATAAGCAGTTCTTCAAAAACTTTGCGCAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	1465 CGCCTGGAAGCTGGCCTAATTGAACCCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1524 1441 AAAGACATCGCTGAAATTGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500	1405 AGCAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAAGGATCAACTTTCCT 1464 1381 CGCCTGGAAGCTCGCCTAATTGAACCCCCCATTTGTGCCAGACCCTTAGTGGTTTATGCC 1440	1345 GAGGAAGCAAAAGTATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1404 1321 AGCAGAGAAAAGTCTGATGATCCCAGGAACAACACTATTTCCT 1380	1285 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1344 1261 GAGGAAGCAAAGAATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320	1225 ATTTATGAAATGGTTGCTGGACGAACACCÁTTCÁAÁGATTACÁÁGGAÁAÁGGTCÁGTÁÁÁ 1284 1201 GAGGATCTGAAGCAACACCACCAAGGGTCAAATTCCAGCATGATAACTTCACA 1260 1201 GAGGATCTGAAGCAAGAACTCTCAAGAAGGTCAAAATTCCAGCATGATAACTTCACA 1260		1081 ATCCTAATGGAAAAGTTAATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140	1021 ATGAAGGSTGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164 1105 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164	AATGTG			781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840				601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660	541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 600	

<i>V</i> 9	D Q	₽ <i>Q</i>	Qy Db	Qy Db	Qy Db	р р	Qy	Qy Db	Qy	Qy Db	Query Match Best Local : Matches 165	ORIGIN	JOURNAL FEATURES	REFERENCE AUTHORS TITLE	VERSION KEYWORDS SOURCE ORGANISM	AR225817 LOCUS DEFINITION ACCESSION	Db	рь Оу
601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660	541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600	481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540	421 GAAGAGCGAGTGGCAGTGAAGGCTGCGCAAGGCTATGGCTTTCTTGCAAGAG 480	361 AACCGCAACCCTTCCTCAGCCAGGCGGGGGCACCAAGTGCGAAGCAGCCACCACTGAG 420	301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360	241 GCCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGGACGC 300	181 GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACGTGCCCACGTTC 240	121 GGGCTGCAGGGCTGCGCCGGAGCTTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180	61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120	1 ATGGTGGACATGGGGGCCCTGGACAACCTGATGGCCAACACCGCCTACCTGCAGGCCCGG 60	Match 99.8%; Score 1655.4; DB 6; Length 1662; Local Similarity 99.8%; Pred. No. 0; Gaps 0;		encoding the Patent: US Loc	Unclassified. 1 (bases 1 to 1662) Walke, D.W., Wilganowski, N.L. and Turner, C.A. Human G-coupled myoteen recentor binases and		AR225817 1662 bp DNA linear PAT 20-DEC-2002 DN Sequence 1 from patent US 6444456.	1705 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTGTTATTG 1743	1645 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1704 1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTTTTTTTT
RESULT	Db Qq	p Q	dg VQ	Ωγ	Qy Db	אַס	Ωy	Db Qy	ОУ Db	Ωу	Qy db	D Q	Db Qy	B 8	}) B &	D 29	Db
11	1621 GAGGGTAATTCATCCAAGTCTGGCGTGTTGTTATTG 1659	1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	1501 GATRAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560 	1441 AAAGACHTGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTTGGAATTTGATGACAAA 1500	1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440	1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380 	1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320 	1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260 	ATTTAT		1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080	961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020	901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960		AAGACC AAGACC	GAAATC	661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720 	601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

. 8	Db Qq	Qy. Db	Qy da	da VQ	Db dd	Qy Db	D QV	Qy Db	Db Qy	QQ dQ	QQ VQ	Query Match Best Local Si Matches 1656;	ORIGIN	JOURNAL FEATURES source	REFERENCE AUTHORS TITLE	SOURCE	VERSION KEYWORDS	AX252439 LOCUS DEFINITION	
661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720	601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAAGATGTATGCCTGTAAG 660	541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAAGGT 600			361 AACCCGCAACCCTTCCTCAGCCAGGCGGGCGCGCCACGTGCCAAGTGCCACCACCCAC	301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360				61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120	1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60	Query Match 99.8%; Score 1655.4; DB 6; Length 1662; Best Local Similarity 99.8%; Pred. No. 0; Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	/organism="nomo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Patent: WC Lexicon Ge I	Halke,D.W., Wilganowski,N.L. and Turner,C.A. Human g-coupled protein receptor kinases and polynucleotides encoding the same	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX252439.1 GI:15985733	AX252439 1662 bp DNA linear PAT 05-OCT-2001 Sequence 1 from Patent WO0168869.	
ACCESSION	RESULT 12 AR263766 LOCUS	סמ	рь	d qq	& B	рь	Q B	AG AG	Q Db	& B	Sy B	δ pp z	OV B	S A S	a da	O B X	o Db	8 8	쿳
AR263766.1 GI:2807574		1621 GAGGGTAATTCATCCAAGTCTGGCGTGTTTTTTTTTTTT	1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCC	1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTT 1561 ATTATGAAAACGGGACTGTTTGAGGAACGATGACCCC	1441 AAAGACATCGCTGAAATGATTGTTCTTCTGAGGTTCGG 1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTT	1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCA	1321 AGCAGAAAAGTCTGATGATCCCAGAAAACATCATTTC 1381 CGCCTGAAGCTGGCCTAATTGAACCCCCATTTGTGCC	1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAG	1201 GAGGAAGCAAAAAAAATATTTGCAAGACGACGAGGTCAAA 1261 GAGGAAGCAAAAAATATTTGCAGCTCTTCTTGGCTAAG	1141 ATTTATGAAATGGTTGCTGGGAACGACCATTCAAAGAT 1201 GAGGATCTGGAAGCAAACTCTTGCAAGACGACGAGGTCAAA	1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACT	ATGAAGG	ATGAAGG	901 GCCTGTGGGATGCTCCACCTCCATGAACTCCACGCATGATGCTCTCGGCACTCCATGAACTCCACGCATGAACTCCACGCATGAACTCCACGTTATCTC	TACAACG	781 AAAACCARCCARCTCTGCCTGTCATGAGCCTGATGAATGGGG 781 TACAACGTGGGCACGCGTGGCCTGGGACATGAGCCGGGTGA		721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTC	661 BBBCTGGBAGAAGCGGCTGAAGAAGAAAGGTGGCGAGA

ATCCAAGTCTGGCGTGTGTTTGTT	B
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1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	뫄
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721 GABATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTGGCCTATGCCCTTTGAGAGC 780				481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540	421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGGCCATGGCTTTCTTGCAAGAG 480	361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACGAGTGCCAAGCAGCAGCACCACTGAG 420	301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360	241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGAG	181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240	121 GGGCTGCAGGGCTGCGCGAAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180	61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGGGGGGG	1 ATGGTGGACATGGGGGCCCTGGACAACCTGATGGCCAACACACGCCCTACCTGCAGGCCCGG 60	Match 99.7%; Score 1654.2; DB 6; Length 1662; Local Similarity 99.8%; Pred. No. 0; es 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	/organism="unknown" /mol_type="genomic DNA"	human kinase Patent: US 6	Ouclassined. 1 (bases 1 to 1662) Guegler, K., Beasley, E.M. and Di Francesco, V. Isolated human kinasa montoing public cold.	
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SOURCE ORGANISM REFERENCE AUTHORS TITLE	LOCUS DEFINITION ACCESSION VERSION KEYWORDS	RESULT 13 AR343544	Дy	B 8	DB QQ	A A	B 84	DB 09	Фb	Db Qy	D 04	g &	Qy Db	Qy Qy	B &	₽ :	OV Db
Unknown. M Unknown. Unclassified. 1 (bases 1 to 1662) Guegler,K., Beasley,E.M. and Di Francesco,V. Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof	AR343544 1662 bp DNA linear PAT 17-AUG-2003 N Sequence 1 from patent US 6579709. RAR343544 AR343544.1 GI:33739257		1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTATTG 1659	1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	1441 AAAGACATCGCTGAAATTGATGATTATCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500	1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440	1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380	1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320	1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260	1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200	1081 ATCCTAANGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCANGGGATGCAGC 1140	1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080	961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGGCCGTGGAG 1020	901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960 	TACAAC	781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC 840

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RESULT 14
AX357902
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ACCESSION AXX
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KEYWORDS
SOURCE HOO
ORGANISM HOO
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TITLE ISS

AX357902 1 from Patent W00192496. AX357902 AX357902.1 GI:18674690

DNA

linear

PAT 13-FEB-2002

Homo sapiens (human)
M Homo sapiens
Eukaryota; Metazoa; Chordata

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Guegler, K., di Francesco, V. and Beasley, E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof Patent: WO 0192496-A 1 06-DEC-2001;
Applera Corporation Robert A. Millman Assistant Secretary (US)
Location/Qualifiers

1. .1662

FEATURES

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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 0;
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AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	RESULT 15 AX166511 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE GORGANISM REFERENCE	Qy 1 Db 1	₽,	Db 15	рь 1 Qy 1		Oy 13	Qy 1	Qy 1 Db 1	Db 12		<i>Qy</i> 1	Qy 1 Db 1
Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clary,D.S. Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 2 31-MAY-2001; Sugen, Inc. (US) Inc. (US) L. 1662 Organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	AX166511 Sequence 2 from Patent WO0138503. AX166511 AX166511 GI:14546856 HOMO sapiens (human) HOMO sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	.621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659 	61	01 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 15	.441 AAAGACATCGCTGAAATTGATGATTTCTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500 .501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	381 CGUCIGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440 441 AAAGACATCGCTGAAATTGATGACTTTCTCTGAGGTTGGGGGGGTGGAATTTGATGACAAA 1500	81 CGCCTGGAAGCTGGCCTAATTGAACCCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGGC 1	.321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380 	.261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGGAACGCTTAGGA 1320 	201 GAGGATCTGAAGCAAAGACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260 	41	 081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140	.021 ATGAAGGTTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Query Match
Best Local Similarity
Matches 1655; Conserv Conservative 99.6%; Pred. No. 0; 0; Mismatches DB 4 6 Length 1662; 0;

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SUMMARIES

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23.5	23.9		25.2	25.2	25.2	25.3	37.2	63.1	66.0	71.6	99.6	99.6	99.7	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	100.0	Match	*
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AAQ87425	AAQ87427	ADB53307	ABK49405	ABL61805	AAQ87426	AAH24842	AAD28072	AAH78798	AAD46351	ABZ56934	ACC44826	AAS06702	AAD28071	AAH78797	ACC44827	AAH78799	ADC39221	ABZ56943	AAD46350	AAD26466	ABQ86178	ABS57375	ID	
			cDNA e	Colon		Nucle		Human	Human		Human	Polyn		Human	Humar	Human	Novel	Human	Human	Human	Novel	Abs57375 cDNA enco		

XPPPXXR

Novel isolated G protein coupled receptor kinase, 69087, nuclear signaling protein, 15821 or mitogen activated protein kinase phosphatase, 15418, useful for treating cellular proliferative or differentiative disorders.

44	44	4 4 2 4 2	41	40	39	38	37	36	ς. ω	34	ယ	32	31	30	29	28	27	26	25	24
151	151	153.4	246.8	253.2	262.4	311.6	311.6	311.6	320.6	320.6	327.2	366.6	368.2	369	373	373	373	373	374.6	377.8
9.1	9.1	ه به د د	14.9	15.3	15.8	18.8	18.8	18.8	19.3	19.3	19.7	22.1	22.2	22.2	22.5	22.5	22.5	22.5	22.6	22.8
2067	2037	3154	1420	1324	2947	1975	1886	1879	2113	2017	3836	2557	2557	1996	2557	2557	2529	2511	2519	2519
σ (an o	00 0	2	N	u	2	N	N	N	N	4.	4	σ	ហ	7	σ	N	N	9	7
AAK99675	ART06290	ACH50623	AAX90222	AAX90223	AAS86360	AAX90220	AAQ75116	AAX90221	AAX90218	AAX90219	ABL19581	AAH24841	ABK49404	AAS80696	ACA56700	AAD36142	AAV71024	AAV71032	ADB47372	ACA03892
Aak99675 2					_					_	_		-		Aca56700 H			Aav71032 G	Adb47372 H	Aca03892 c
2067nt hu	Human sig	Human mam	GRK4 poly	42	DNA encod	GRK4 polv	Composite	GRK4 poly	GRK4 poly	GRK4 poly	Drosophil	Nucleotid	cDNA enco	DNA encod	Human siq	Human G p	Grk5-gree	Grk5-gree	Human cDN	cDNA upre

ALIGNMENTS

RESULT	Fig. 1
ABS57375	7375
¥	ABS57375 standard; cDNA; 2198 BP.
AC	ABS57375;
X	
žä	04-FEB-2003 (first entry)
	cDNA encoding human GPCR kinase (GPCRK) 69087.
₹ \$	Himan: G protein compled receptor bispect concer
KW	cellular proliferative disorder; differentiative disorder:
W	haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;
ğ	metastatic disorder; cytostatic; gene therapy; gene; ss.
	Homo sapiens.
꼭 X	Key Location/Qualifiers CDS 2911952
	_
X II II I	<pre>/product= "GPCRK 69087" /note= "The coding sequence given as SEQ ID No:3 is specifically claimed in Claim 1"</pre>
PN	US2002123464-A1.
X 23 3	05-SEP-2002.
Y P	22-OCT-2001; 2001US-00044205.
PR	
	20-OCT-2000; 2000US-0241877P. 23-OCT-2000; 2000US-0242428P.
Y PA	(MILL-) MILLENNIUM PHARM INC.
	Kapeller-Libermann R, Bandaru R;
	WPI; 2003-066811/06.

Claim 1; Fig 1; 98pp; English.

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neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic disorders). They are also useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The sequences may also be used to screen public databases to identify other family members or related sequences. The polypeptide sequences are useful as immunogens to generate antibodies that bind the polypeptides. The polypuclective genes on a chromosome, identifying gene regions associated with cellular proliferative or differentiative disorders, and in gene therapy. The present sequence encodes human GFCRK 69087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of a novel human G protein coupled receptor (GPCR) kinase (GPCRK) designated 69087), a novel human nuclear signalling protein designated 1581, and a novel human nuclear signalling protein kinase (MAPK) phosphatase MAPKP designated 15418, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating and disgnosing disorders such as cellular proliferative and differentiative disorders (e.g. haematopoietic neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic
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Query Match
100.0%; Score 1659;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other; DB 7; Length 2198;

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Indels

0; Gaps

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720	AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAAG	661	₹ 0
950	GTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG	891	뮍
660		601	Ş
068		831	망
600	TTCGAGATGCAACCAGTGTCAGAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT	541	Ş
830		771	Дb
540		481	Qy
770		711	DЬ
480	GAAGAGCGAGTGGCTGCAGTGACGCCTGACGCCAAGGCCATGGCTTTCTTT	421	8
710		651	Db
420	AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG	361	Ş
650		591	Дb
360	ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCCACTTGTGCGAGTGCCCCTGCCCCCGGGG	301	Qy
590		531	뫄
300	CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGAGGGAG	241	Ş
530		471	밁
240	GAGCAGCAGCCCATCGGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC	181.	Ş
470	GGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 4	411	DЪ
180		121	Ş
410	AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCC 4	· 351	윩
120		61	Ş
350	ATGGTGGACATGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG	291	B
60		1	Ş

1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659	Q Q
1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG	Qy Db
1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1	gg Qy
441 AAAGACATCGCTGAAATTGATGATTCTCTGAGGTTCGGGGGGTGGAATTTGATGA 	D Qy
1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1	Ag Ag
1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1 	4g 4g
1261 GAGGAAGCAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1	D Qy
1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1 	Dy dy
ATTTAT	QУ
1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1	ob VQ
021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGC:	D- Qy
1 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCC 	Qy db
901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 9	Qy Db
#=#	Qy
781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840	DD Qy
GAAATCTTGGAGAAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTT	db Qy
CTTGGA	Db

RESULT 2
ABQ86178
ID ABQ8
XX
AC ABQ8

ABQ86178 standard; DNA; 1662 BP.

ABQ86178;

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cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, amorectic, and metabolic. Polypeptides and polynucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neophastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, hyperproliferation, systemic autoimmune disease, hyper-immunity, developmental abnormality, gastrointestinal ulceration, neuropathy, haematological diseases, metabolic diseases, sperm dysfunction, thyroid diseases, sperm dysfunction, thyroid
                disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
transduction deficiency, neurological diseases, stroke, angiogenes
                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. Activity of polypeptides of the invention may be described as,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-2001;
04-APR-2001;
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20-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                        Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                                                                                                          Claim 2(a); Page 255-256; 335pp; English.
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(SMIK )
(GLAX )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism, brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart trachea; thymus; lymph node; muscular system; obesity; anorexia;
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30-JAN-2001;
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SMITHKLINE
GLAXO GROUP
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       disorders,
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SA, Rizvi SK,
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2001US-0264922P

2001US-026797P

2001US-0276988P

2001US-0281535P

2001US-0289622P
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2000US-0257048P.
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rum JC, Xie
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                                                                                             AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC
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                    TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA
                                                                             AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC
                                                                                                                                  GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
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                                        Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirribosis; Cushing's syndrome; hepatitis; hypothyroidism, cerebral palsy; catearact; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; congestive heart failure; ischaemic heart disease; lung tumour; gout;
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                           fatty liver; Niemann-Pick's disease; gene
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Score 1655.8; Pred. No. 0; Mismatches

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Gaps

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Sequence 1662

BP; 420 A; 411 C; 479 G; 352

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CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bornchitis, Crohn's disease, diabetes autoimmune thyroiditis, gout, bornchitis, Crohn's disease, diabetes CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative collitis, CC prowth and development disorders (arteriosclerosis, cirrhosis, hepatitis, CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio CC vascular disease (arteriovenous fistula, hypertension, vasculitis, CC aneurysms, congestive heart failure, angina pectoris, myocarditis, CC disorder (fatty liver, Fabry's disease, Niemann-pick's disease, CC hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity CC of a test compound and in gene therapy. The present sequence is human CC of the compound and in gene therapy. The present sequence is human compound.
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23-JUN-2000; 2000US-0213467P.
30-JUN-2000; 2000US-0215651P.
07-JUL-2000; 2000US-0216605P.
13-JUL-2000; 2000US-0218372P.
25-AUG-2000; 2000US-0228056P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing pKIN agonist is useful for treating a disease or condition associated with decreased expression of pKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of pKIN. The disease or condition associated with overexpression of pKIN. The disease or condition associated with overexpression with the proposed pkin and the protein associated with overexpression of pKIN. The disease include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder protein and the pKIN agonist is useful for treating a disease or condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides, useful for diagnosing, treating or preventing died growth and development, cardiovascular and lipid, and diseases cancer, comprise human kinase polypeptides.
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                                                                                        ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
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                                                        ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
                                                                                                                                                                                                                                                  GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
                                                                                                         ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
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                                                                                                                                                                                                                                                                                                                          AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA
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(first entry)

Human cone opsin kinase (GRK7) cDNA.

Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7; GRK7; cone visual signalling; visual sensitivity; visual resolution; night blindness; colour blindness; Oguchi disease; Pineal gland activity; chronobiological desynchrony; depression; anxiety; memory loss; headache; mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological; gene therapy; antidepressant; analgesic; gene; ds.

07-MAR-2002; 2002WO-US007025

GRK7

protein"

07-MAR-2001; 2001US-0274006P

Mosley BA;

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Identifying compounds that alter inhibition of cone opsin kinase polypeptide activity for treating a conditions related to cone visual signaling, comprises mixing a compound with a cone opsin kinase and with an inhibitory polypeptide.

Example 4; Page 45-46; 6lpp; English.

The present invention relates to novel human cone opsin kinase (G-protein coupled receptor kinase 7; GRK7) and their corresponding polymucleotides. The invention further relates to a method of identifying compounds that calter the inhibition of GRK7 polypeptide activity which involves mixing a contest compound with GRK7 protein and an inhibitory polypeptide and cativity by the inhibitory polypeptide. GRK7 sequences are useful for treating conditions related to come visual signalling (e.g., night cativity by the inhibitory polypeptide. GRK7 sequences are useful for treating conditions related to come visual signalling (e.g., night cativity by the inhibitory polypeptide. GRK7 sequences are useful for the singular conditions related to come visual signalling (e.g., night cativity, visual resolution or in adapting to changes in light cativity, visual resolution or in adapting to changes in light cativity. Outh disease or dominant congenital stationary night cativity (e.g., chronobiological desynchrony, cativity (e.g., chronobiological desynchrony, cativity (e.g., chronobiological desynchrony, cativity (e.g., chronobiological desynchrony, cativity is beneficial, e.g., decreased colour sensitivity or other cone cativity is beneficial, e.g., decreased colour sensitivity or other cone photoreceptor wisual signalling or circadian rhythm, as molecular to come photoreceptor visual signalling or circadian rhythm, as molecular cand vision resolution. They are also used as gene therapy tools for and vision resolution. They are also used as gene therapy tools for individuals with such disorders. The present sequence is human GRK7

Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 1657; Conserv

Conservative

0; Mismatches Score 1655.8; Pred. No. 0;

2; Indels

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0

99.8%;

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Length 1662;

밁 Ş В 망 301 181 481 481 421 421 361 361 301 241 241 181 121 121 5 61 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT | CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGGTAGCCTGGCCCC ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC GGGCTGCAGGGCTGCGCGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCCATGGCTTTCTTGCAAGAG GAAGAGCGAGTGGCTGCAGTGAGCCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAACTGCCAAGTGCCAAGCAGCACCACTGAG 420 ACCANAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCCTGCCCCGGGG CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGCTGGCCGAGGAGGACCCC GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240 180 180 120 120 60 60 360 300 300 540 480 480 420 360

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1 AAAGACATCGCTGAAATTGATGATTCTCTGAGGTTCGGGGGGGTGGAATTTGATGACAAA 15	144	Вb
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COCCUTORA AGCUTOZOCUTA AUTUGA ACCCCCATUTOGTOCCAGACCCCTTCAGTOGTTTATGCC 1	1 0	? ;
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1 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 13	126	ఠ
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L GAGGATCTGAAGAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1	120	В
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L ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1	114	Ş
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1 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080	102	뮹
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ANGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG	96:	뭥
AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGGCTGGCCGTGGAG 1	96:	\$
1 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960	90:	밁
GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAG	903	Ş
1 TACAACGTGGCCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900	84:	ద
TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCC	84.	γQ
1 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAGTGGGGGAGACCTCAAGTTCCACATC 840	787	Db
AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACAT	78:	8
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GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC	721	Ş
AACTGGACAAGAAGCGGCTGAAGAAGAAGATGGCGAGAAGATGGCTCTCTTGGAAAA	661	Вb
AAGAAAGGTGGCGAGAAGATGGC	661	γQ
TATGCCTGTAA	603	뭥
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel disease associated gene and its uses. The gene and its encoded protein are useful for diagnosis of and screening for drugs for heart diseases, cancers and omentopathy. The current sequence represents a human gene sequence relative to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel disease-associated gene of the RGS gene family and its product, applicable in diagnosis of and screening for drugs for heart diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 85-86; 96pp; Japanese.
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CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC
                                          GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC
                                                            GAGCAGCAGCACCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC
                                                                                                                    GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
                                                                                                                                                         AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC
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99.9%; Pred. No. 0;
tive 0; Mismatches 2; Indels 0;
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                                                                GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
                                                                                                        GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA
          AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT
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                                                GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA
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                                              15-MAY-2001;
16-MAY-2001;
18-MAY-2001;
21-MAY-2001;
22-MAY-2001;
23-MAY-2001;
25-MAY-2001;
29-MAY-2001;
29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2001;
03-MAY-2001;
07-MAY-2001;
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                                                                                                                                                                                                                                                                                     11-MAY-2001;
14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                        09-MAY-2001;
09-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hemophilia; graft-versus-host disease;
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; 2001US-0288063P.

2001US-028939SP.

2001US-028908TP.

2001US-0299818P.

2001US-0290194P.

2001US-0290154P.

2001US-0290754P.

2001US-0291181P.

2001US-0291243P.

2001US-029200TP.

2001US-029200TP.

2001US-029374P.

2001US-0293107P.

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dadcadcadcccarcedredcccccrrrccdrdacrrccradccacadrdcccacdrrc 312 GAGCAGCCACCCCCCCCCCTCTTCCCTAGCCACAGTGCCCACAGTGCCCACGTTC GGGCTGCAGGGCTGCGGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT GGGCTGCAGGCTGCGCGGAGCTCCCGCCAGAAGCTGTCCCCTGAACTTCCACAGCCTGTGT Ś 片 S

Matches Query Match

1657;

Conservative

0

Local

Similarity

99.8%;

Score 1655.8; Pred. No. 0; Mismatches

DB 9; 2

1821; 0: Gaps

Indels Length

0

Sequence 1821

BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;

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AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGCGTAGCCTGGCCCTGCCC AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG ATGGTGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG

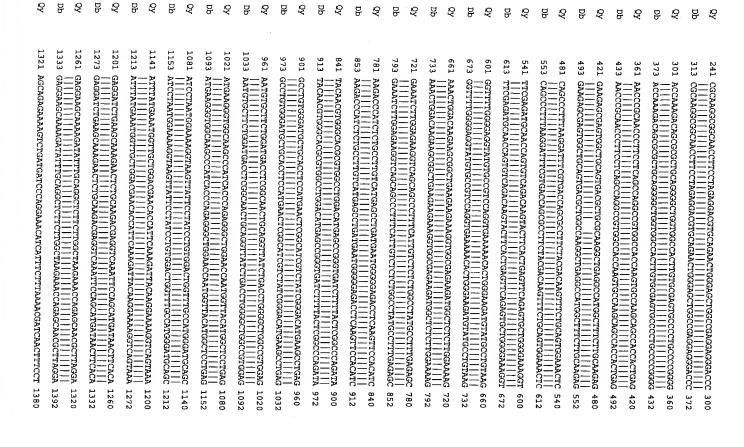
180

252

240

120 132 60

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The invention relates to new isolated NOVX polypeptides, the genes coding them or sequences having at least 95% identity to the amino acid cor nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated correcting, preventing or alleviating pathology associated with NOVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NOVX colypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide are especially useful for treating or preventing e.g. colypeptide are especially useful for treating or preventing e.g. colypeptide are especially useful for treating or preventing e.g. cancer; disbetes, obssity, cancers (e.g. lymphoma, uterus cancer or prostate completes, dyslipidemias, amorexia, wasting disorders, Alzheimer's disease, carkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's conditions to disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's conditions the protein is useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for conditional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX genes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2001; 2001US-0304879P.
31-JUL-2001; 2001US-03108901P.
14-AUG-2001; 2001US-0312270P.
17-AUG-2001; 2001US-0313416P.
10-SEP-2001; 2001US-0313463P.
27-SEP-2001; 2001US-0313929P.
28-NOV-2001; 2001US-033092P.
28-NOV-2001; 2001US-033092P.
03-DEC-2001; 2001US-033593P.
03-DEC-2001; 2001US-033552P.
21-FEB-2002; 2002US-0359245P.
21-FEB-2002; 2002US-0359245P.
01-MAY-2002; 2002US-00136626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller CE, Kekuda R, Malyankar UM, Li L, Pena CEA, Spytek KA; Gorman L, Guo X, Fernandes ER, Smithson G, Stone DJ, Zerhusen BD; Patturajan M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR; Padigaru M, Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, Zhong Edinger SR, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 165; 748pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with a human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
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	B 8	A 4	B &	B &	B 8	Db
	1621 1693	1561 1633	1501 1573	1441 1513	1381 1453	1393
	GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659			AAAGACATCGCTGAAATTGATGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA	CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC	

AAH78799 RESULT 7

AAH78799 standard; cDNA; 2249 ₽₽

ААН78799;

08-MAR-2002

(first entry)

Human G-protein coupled receptor kinase 3 cDNA sequence

drug screening; gene novel human protein. G-protein coupled receptor kinase; GRK; human; ss; gene therapy; gene expression characterisation; NHP,

Homo sapiens.

WO200168869-A2

20-SEP-2001.

08-MAR-2001; 2001WO-US007500

10-MAR-2000; 2000US-0188449P

Walke DW, (LEXI-) LEXICON GENETICS INC.

Wilganowski NL,

Turner CA;

2001-570872/64.

New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological

Disclosure; Page 33-34; 34pp; English.

The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRX), also designated NHP (novel human protein) in the specification, which is shown in the sequence listing. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides derived from the nucleotides of the invention are useful as hybridisation probes for screening libraries and assessing gene expression patterns. The nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRK expression. The nucleotides of the invention can be used to genetically engineer host cells to express GRK products in vivo. The nucleotide sequences of the invention are also useful in addressable arrays for identifying and characterising the

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;
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                TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTTACTCGGCCCAGATA
                                                                               AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATC
                                                                                                                         GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
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Db	Qy	D D	Qy	В	Qy	Db	8	Dβ	φ	Δb	Qy	Db	Ş	Db	Qγ	рb	γQ	Db	80	Db	γ0	Db	γQ	Дb	8
1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTATTG 2012	1621 GAGGGTAATTCATCCAAGTCTGGCGTGTTTTTTTTTTTT	1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973	1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	1854 GATBAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913	1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853	1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500	1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCCTTCAGTGGTTTATGCC 1793	1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440	1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAAACGATCAACTTTCCT 1733	1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380	1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673	1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320	1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613	1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260	1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAAGGTCAGTAAA 1553	1141 ATTTATGAAATGGTTGGTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200	1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTTGCCATGGGATGCAGC 1493	1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140	1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433	1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCCAATGGTTACATGGCTCCTGAG 1080	1314 AATGIGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGGTGGCCGTGGAG 1373	961 AATGIGCITCIGGATGACCICGGCAACIGCAGGITATCIGACCIGGGGCTGGCCGIGGAG 1020	1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGGACATGAAGCCTGAG 1313	901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

ACC44827

standard; cDNA; 3186 ΒP

04-JUN-2003 (first entry)

Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.

Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic; neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant; vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder; central nervous system disorder; reardiovascular disorder; asthma; COPD; chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme; Alzheimer's disease; Parkinson's disease; congestive heart failure; myocardial infarction; ischaemic disease; hypertensive vascular disease;

Homo

sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human G protein-coupled receptor kinase (GRX) protein (I). (I) has cytostatic, antidiabetic, neuroprotective, nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and antiasthmatic activities, and can be used in gene therapy. (I) can be regulated to treat cancer, diabetes, a central nervous system (CNS) disorder (e.g. anxiety or mood disorders, Alzheimer's disease and Parkinson's disease), cardiovascular disorders (e.g. congestive heart failure, myocardial infarction, ischaemic diseases of the heart or hypertensive vascular disease), asthma and chronic obstructive pulmonary disorder (COD). GRX molecules are useful in screening for agents that regulate or decease the activity of a GRX. GRX sequences may also be used for determing diseases and abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3186 BP; 857 A; 737 C; 784 G; 808 T; 0 U; 0 Other;
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85. .1746
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                          CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
                                                                                          AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT
                                                                                                                                     GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA
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The present cDNA sequence encodes a human G-protein coupled receptor CC kinase (GRK), also designated MHP (novel human protein) in the Specification, which is claimed in the invention. The invention comprises CC novel human nucleotide and protein sequences which have similarity to G-cc novel human nucleotide and protein sequences which have similarity to G-cc nucleotides of the invention are useful as hybridisation probes for CC corrections of the invention are useful as hybridisation probes for CC correctides of the invention are also useful in drug screening and gene CC therapy for the modulation of GRK expression. The nucleotides of the CC invention can be used to genetically engineer host cells to express GRK CC products in vivo. The nucleotide sequences of the invention are also useful in addressable arrays for identifying and characterising the cc temporal and tissue specific expression of a gene and in microarrays to.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological
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                                                                                                                                                             Human kinase cDNA.
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The invention relates to human kinase proteins that are related to G-CC protein coupled receptor kinase subfamily. Human kinase gene is located CC on chromosome 3. The kinase peptide and nucleic acid are useful in the CC development of human therapeutic and diagnostic compositions. The peptide CC valuable to the field of pharmaceutical development to identify and cC characterise modulators of the kinase. The proteins may also be used to CC raise antibodies or to elicit an immune response, as a reagent in assays CC designed to quantitatively determine levels of the protein in biological CC preferentially expressed (either constitutively or at a particular stage CC kinase proteins are also useful for providing a target for diagnosing a cdisease or predisposition to disease mediated by the peptide. The nucleic acid molecules are useful for probes, primers, chemical intermediates and CC in biological assays. The nucleic acids are also useful in making vectors containing the gene regulatory regions of the nucleic acid molecules and cfor drug screening to identify compounds that modulate kinase nucleic containing the gene regulatory regions of the nucleic acid molecules and ccid expression. The present sequence is human kinase cDNA expressed in Skins, germinal center B cells, colon, kidney and lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human kinase proteins and nucleic acids, useful as a major target for drug action and development, particularly for screening modulators of the kinase peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 1; 87pp; English.
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18-DEC-2000;
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Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;

DB 6; Length 1662;

밁 Ś 밁 Ś 밁 Ś 밁 S よ Ś 밁 Ş Matches 1656; Query Match Best Local Similarity 301 241 241 181 181 GAGCAGCACCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 121 121 GGGCTGCAGGGCTGCGGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGGCTGTGT 180 61 61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120 CGCAAGGCGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCCC ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCCTGCCCCGGGG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG GGGCTGCAGGGCTGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCCGCCTACCTGCAGGCCCGG AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC Conservative ZAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCC 99.78; 99.88; ·, Score 1654.2; Pred. No. 0; Mismatches υ •• Indels ٥, Gaps 360 360 300 300 240 240 180 120 60 60 0

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00	TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 6	541	B
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٠	1621 GAGGGTAATTCATCCAAGTCTGGCCTGTGTTTGTTATTG 1659	1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTTGTTATTG 1659	1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	1561 ATTATAGAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620	1501 GATRAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560	

RESULT 11 AAS06702 AAS06702 standard; cDNA; 1662 BP AAS06702;

Polynucleotide sequence encoding human protein kinase #2

12-SEP-2001

(first entry)

Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.

Homo sapiens.

WO200138503-A2

31-MAY-2001

22-NOV-2000; 2000WO-US032085

24-NOV-1999; 99US-0167482P

(SUGE-) SUGEN INC.

Plowman GD, Flanagan P, Whyte Clary ם מ Manning G, Sudarsanam S, Martinez R;

WPI; 2001-343950/36. P-PSDB; AAU03502.

Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.

Example 1; Fig 1; 433pp; English.

AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel CC protein kinases have been identified as members of the tyrosine or CC serine/threonine kinase (PTK and STK) families. The polymucleotides concoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with the protein kinase expression. For example, they may be used to treat concers (e.g. atherosclerosis), metabolic diseases (e.g. diabetes), disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), concers (e.g. schizophrenia), neurodegenerative disorders (e.g. firemune related diseases (e.g. rheumatoid arthritis), neurological confiders (e.g. schizophrenia), neurodegenerative disorders (e.g. firemune related productive disorders (e.g. asthma), infectious confiders (e.g. schizophrenia), neurodegenerative disorders (e.g. asthma), and reproductive disorders (e.g. infertility). Additionally, polymucleotides encoding protein kinases may be used for conjupeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of control kinases and as NMA probes and as assays to identify modulators of control kinases and in assays to identify modulators of control kinases and in assays to identify modulators of control kinases and in assays to identify modulators of control kinases and in assays to identify modulators of control kinases and in assays to identify modulators of control kinase and as NMA probes and in assays to identify modulators of control kinases and in assays to identify modulators of control kinase and as many activity. protein kinase expression and activity

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         AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG
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Pred. No. 0;
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                                                 "G protein-coupled receptor kinase (GRK)"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder (e.g. anxiety or mood disorders, Alzheimer's disease and Parkinson's disease), cardiovascular disorders (e.g. congestive heart failure, myocardial infarction, ischaemic diseases of the heart or hypertensive vascular disease), asthma and chronic obstructive pulmonary disorder (COPD). GRK molecules are useful in screening for agents that regulate or decease the activity of a GRK. GRK sequences may also be used for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a human G protein-coupled receptor kinase (GRK) protein (I) (I) has cyrostatic, antidiabetic, neuroprotective, nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and antiasthmatic activities, and can be used in gene therapy. (I) can be regulated to treat cancer, diabetes, a central nervous system (CNS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 71.6%; Score 1187.8; DB 7; Length 1191; Best Local Similarity 99.8%; Pred. No. 3.7e-286; Matches 1189; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel disease associated gene and its us. The gene and its encoded protein are useful for diagnosis of and screening for drugs for heart diseases, cancers and omentopathy. The current sequence represents the human RGSNO9 encoding DNA sequence
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Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7; GRK7; cone visual signalling; visual sensitivity; visual resolution; night blindness; colour blindness; Oguchi disease; Pineal gland activity; chronobiological desynchrony; depression; anxiety; memory loss; headache; mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;

Human cone opsin kinase (GRK7) OK6 splice variant cDNA.

27-JAN-2003

(first entry)

gene therapy; antidepressant; analgesic; gene; ds.

CDS

Location/Qualifiers
1. .1062

/*tag=

/product= "Human GRK7 OK6 splice variant protein"

Homo sapiens.

07-MAR-2002; 2002WO-US007025

19-SEP-2002. WO200272541-A2

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S
                                                                                                                                                                                    cc sensitivity, visual resolution or in adapting to changes in light cc intensity, Oguchi disease or dominant congenital stationary night continuess), Pineal gland activity (e.g., chromobiological desynchrony, cc depression, anxiety, mental fogginess, memory loss, headaches, fatigue, cc or jet lag). Agonists of GRK7 polypeptide activity may be used to treat cc activity is beneficial, e.g., decreased colour sensitivity or other come photoreceptor mediated diseases. The GRK7 proteins are also useful in the cc preparation of a medicament for treating a condition or disease related cc preparation of a medicament for treating a condition or disease related cc probes to screen for inherited defects in colour vision, circadian rhythm as molecular crows and vision resolution. They are also used as gene therapy tools for condition with such disorders. The present sequence is human GRK7 OK6
                                                              Matches 1381; Conservative
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human cone opsin kinase (G-protein coupled receptor kinase 7; GRK7) and their corresponding polynucleotides. The invention further relates to a method of identifying compounds that alter the inhibition of GRK7 polypeptide activity which involves mixing a test compound with GRK7 protein and an inhibitory polypeptide and determining if the test compound alters the inhibition of GRK7 protein activity by the inhibitory polypeptide. GRK7 sequences are useful for treating conditions related to cone visual signalling (e.g., night blindness, colour blindness, difficulty with colour vision, visual blindness, colour blindness, difficulty with colour vision, visual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying compounds that alter inhibition of come opsin kinase polypeptide activity for treating a conditions related to come visual signaling, comprises mixing a compound with a cone opsin kinase and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-723307/78.
P-PSDB; AAE28953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2001; 2001US-0274006P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an inhibitory polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 48-49; 61pp; English
                                                                                                                                  Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;
1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spencer M,
                                                                                66.0%;
83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mosley BA;
                                                            Score 1094.2; DB 6; Length 1486; Pred. No. 9.5e-263; O; Mismatches 3; Indels 275;
                                                                  Gaps
                                  60
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1050

1081 AICCIAAIGGAAAAGGIAAGAAAAAAAAAAAAAAAAAAA	γQ
601	2
Р	Db
1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTTGGAACCAATGGTTACATGGCTCCTGAG 1080	Ş
10	Db
02	Qy
ATGAAGCCTGAG 960	dd
. 6	S S
841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900	Db
841 TACAACGTGGGCACGTGGCCTGGACATGAGCCGGGTGATCTTTTTACTCGGCCCAGATA 900	Qy
	Db
781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGGAACCCTCAAGTTCCAACATC 840	γο
	Db
721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGGCCTATGCCTTTGAGAGC 780	Ωγ
661 ABACTGGACAAGBAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720	DЬ
661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTTGGAAAAG 720	Qy
601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660	ממ
601 GGTTTTGGGGAGGTATGTGCCGTCCACGTGAAAAACACTGGGGAAGATGTATGCCTGTAAG 660	8
60	Db
541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600	δ
u	מת
481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540	Qy
421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCCATGGCTTTCTTGCAAGAG 480	Ф
421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCCATGGCTTTCTTGCAAGAG 480	Qy
361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCCACCACTGAG 420	Db
361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAACTGCCAACCAGCCACCACTGAG 420	γQ
301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCCTGCCCCGGGG 360	ΔD
301 ACCAAAGACAGCGCCTGCAGGGGGCGCTGGTGGCCACTTGTGCCGAGTGCCCCTGCCCCGGGG 360	Q
241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300	Db
241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACGGAC	Ø
181 GAGCAGCCATCGGTCGCCGCCTCTTCCGTGACCTTCCTAGCCACAGTGCCCACGGTTC 240	Db
181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240	γQ
121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAAGCTTCCACAGCCTGTGT 180	DЬ
121 GGGCTGCACGGGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180	Qy
61 AAGCCCTCGGACTGCGACAAGAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120	Db
61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120	Qγ
1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60	Db

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RESULT 15
AAH78798
ID AAH788
XX AAH788
XX AAH788
AC AAH78
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   WPI; 2001-570872/64.
P-PSDB; AAG77816.
                                                                                           Walke DW,
                                                                                                                                                                                                                                                             08-MAR-2001; 2001WO-US007500
                                                                                                                                                                                                   10-MAR-2000; 2000US-0188449P
                                                                                                                                                                                                                                                                                                                                                                                   WO200168869-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor kinase; GRK; human; ss; gendrug screening; gene expression characterisation; NHP;
                                                                                                                                         (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G-protein coupled receptor kinase 2 cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH78798 standard; cDNA; 1062 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
                                                                               Wilganowski NL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGCCTAGGGGTTGTGAG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGACATCGCCGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           product= "G-protein coupled receptor kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1062
                                                                                  ÇĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1285
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mulectides of the invention are useful as hybridisation probes for coreening libraries and assessing gene expression patterns. The nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRIK expression. The nucleotides of the convention can be used to genetically engineer host cells to express GRIK convention can be used to genetically engineer host cells to express GRIK convention are also the convention are also convention in addressable arrays for identifying and characterising the convention are conventional and tissue specific expression of a gene and in microarrays to conventional medical condition. The proteins of the invention are useful conventional medical condition. The proteins of the invention are useful conventional patterns who have a conventional medical condition. The proteins of the invention are useful conventional patterns who have a conventionaly conventional patterns who have a conventional patterns who have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NHP (novel human protein) in the specification, which is claimed in the invention. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding human proteins that share sequence similarity with animal kinases e.g. G-protein coupled receptor kinases, useful for drug screening, diagnosis and in gene therapy of biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 32; 34pp; English.
                                                                                                      las reagents
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Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;

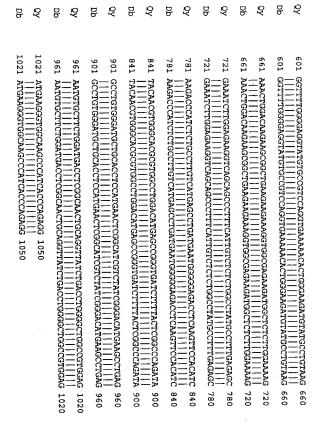
Query Match Best Local

Similarity

Score 1046.8; DB 4 Pred. No. 5.6e-251;

DB 4; Length 1062

δÃ 밁 Ş 밁 S 뮹 Ş 밁 S 뫄 Ş 밁 Ş 片 Ş 밁 γQ 片 Ś Matches 1048; 481 481 421 361 361 301 301 421 241 181 241 181 121 121 13 61 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC GAAGAGCGAGTGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCCAAGTGCCAAGCAGCCACCACTGAG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACCC CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGACGCC GAGCAGCAGCCCATCGGTCGCCCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCC 120 ATGGTGGACATGGGGGCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60 GAGCAGCATCGATCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC GGGCTGCAGGGCTGCGGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 63.1%; ilarity 99.8%; Conservative 0; Mismatches Indels 0; Gaps 600 540 180 540 480 480 420 420 360 360 300 300 240 240 180 60 0



Search completed: August 13, 2004, 14:01:08 Job time : 450.751 secs

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Result
No.
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                398.6
375
311.8
311.6
                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                     EST:*

1: em
2: em
3: em
5: em
7: em
9: gt
110: g
111: g
112: g
111: g
114: g
115: g
116: g
122: g
123: g
124: g
125: g
126: g
127: g
128: g
1
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Match Length DB
                24.0
22.6
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18.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atggtggacatgggggccct.....ctggcgtgtgttttgttattg 1659
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1659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_htc:*
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Please visit our web site for further details.
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/clone_lib="RIKEN full-length (
/dev_stage="12 days embryo"
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                                              /note="G PROTEIN-COUPLED RECEPTOR KINASE GRK6 (EC 2.7.1.-) homolog [Mus musculus] (SWISSPROT|O70293, evidence: FASTY, 100%ID, 96.9%length, match=1714)
                                                                                                                                                                                                                                               /db_xref="FANTOM_DB:D130046K22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 GGCGCCAGATGCTGCAGTTCCCCCCATATCAGCCAGTGTGAGGAGCTTCGACTCAGCCTTG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAGTTTCTGCAGTGGAAACTCTTCGAGAGGATGCAACCAGTGTCAGACAAGTACTTCACTG 577
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CTGTGGGCTACATGGCTCCAGAGGTGGTGAGG---AATGAGCGCTACACGTTCAGTCCTG
                                                                                                             CGGACCTGGGACTGGCATGTGCCTGAGGGCCAGACCATCAAAGGCCGTGTGGGCA
                                                                                                                                                         CTGACCTGGGGCTGGCCGTGGAAAGGTGAAAGGCTAAGCCCAGAGGGCTGGAA 1057
                                                                                                                                                                                                                        TGTACAGGGATCTAAAGCCAGAGAATATCCTTCTGGATGACCATGGCCACATTCGGATCT
                                                                                                                                                                                                                                                                       TCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTAT
                                                                                                                                                                                                                                                                                                                                   CTGTCTTCTATGCTGAGATCTGCTGTGGCCTGGAAGACCTGCACCGGGAACGCATTG
                                                      CCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGG 1117
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Consortium (LLNL)

Priscilla Furth

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1538
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                  Direct Submission
Submitted (29-AUG-2003) National Institutes of Health, N
Gene Collection (MGC), Cancer Genomics Office, National
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                                                                                                                       Strausberg, R.
                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                 numan and mouse cDNA sequences
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372 CTTCCTCAGCCAGGCGTGGCCACCAAGTGCCAGCCACCACTGAGGAAGAGGGAGT 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAK Plate: 123 Row: m Column: 10
This clome was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 7
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akhter, N., Ayele, K., Beckstrom Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R.W., Bouffard, G.G., Breen, K., Haghighi, P., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Lothar Hennighausen Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
                                                                                                                                                       CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC
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                                                                                              TGGGCGCC---GACTAATGCAGAACTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="NMRI"
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/lab_host="DH10B"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgi-bin/cluster.cgi?seq=CSOAA004AG03NP1&cluster=3090.f. Contact Feng Lidang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSOAA004AG03NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3090.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX404586.1 GI:30648023
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CATGGCGCTGAACGAGAAGCAGATCCTCGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTT
                                       GATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCT
                                                                               TAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAAGGC 825
                                                                                                            GAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGCTGAAGAAAGGTGGCGAGAA 701
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                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NcI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CS0DA004YM05"
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                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                              Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Pa
                                                                                                                                                                                                                                                                                                                                             BC027597
2329 bp mRNA linear HTC 01-HOMO sapiens, Similar to G protein-coupled receptor kinase (Drosephila), clone IMAGE:4830673, mRNA.
                                                                                                                                                                                           Strausberg, R.
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                                                                                                                      Institute,
                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                Homo sapiens (human)
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            Library Preparation: Michael J.
                                                                                                                   31 Center Drive, Room 11A03,
                           Palkovits, M.D., Ph.D.
           Brownstein (NHGRI) &
                                                                                                                   Bethesda, MD 20892-2590,
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through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 34 Row: i Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885346 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution
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Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology
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TGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATG 1136
                                                                                                               AGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTACATGGCACC
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/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 5.5e-60;
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                                                                                                                                                                                                                                                                 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3090.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                   cgi-bin/cluster.cgi?seq=CSOBAI046ZH12_CS04416_1&cluster=3090.f.
CONTECT: Feng Liang Email: fliang@llfetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen.comporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAI046ZH12_CS04416_1.
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BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODDO10YD11"
/cell_type="B_CELLS_(RAMOS_CELL_LINE)
/cell_line="RAMOS_CELL_LINE"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
                    25-NORMALIZED"
                                  'clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (human)
                                lib="Homo sapiens B CELLS (RAMOS CELL LINE)
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                                                              AY406080:1 GI:39762054
GSS:
                                                                                           genomic survey sequence.
AY406080
                                                                                                                             Homo sapiens GPRK5 gene,
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                           Homo sapiens
                                                                                                                                             AY406080
                                            Homo sapiens (human)
                                                                                                                                                                                                                                GAGGAAGAAGATCAAGCGGGAGGAGGTGGAGC 45
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1721 bp VIRTUAL

DNA

linear

GSS 15-DEC-2003

TRANSCRIPT, partial sequence,

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459 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 518
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                                                                                                                                                                                                                                                                                                GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC
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                                                                                                                                                                                               TGACCTGGGACTAGCTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCAC
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Pred. No. 3.7e-59;
0; Mismatches 270
                                                                                                      -GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGA
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal, Frod,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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                                                                                                                                                                                                                                                                                                                                     AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTAT 821
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S 밁 Ś 맔 Š 망 8

/organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon:9606"
/clone="TMAGE:5813090"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"

1. .1058

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1476 NNNNNNNNNNNNNNNNNATGATÄGAÄÄCAGAÄTGCTTTAÄGGÄGCTGÄÄCG 1524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1366 ACGATCAACTITCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCT 1425
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found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LLCM2064 row: j column: 03
High quality sequence stop: 631.
Location/Qualifiers
                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Standt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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/clone_lib="NIH_MGC_99"

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459 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 518
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BQ061148 1019 bp mRNA linear EST 02-APR-2002 AGENCOURT_6862941 NTH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BQ061148
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EST.
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Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2083 row: h column: 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                  GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGGCCTGGACATGAGCCGGGT 878
                                                                                                    CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG
                                                                                                                                          TCTGGCCTATGCCTTTGAGAGCCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 818
                                                                                                                                                                                                                                                                                                                                                             TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAGGTGGCGA 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue type="lymphoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
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/db_xref="taxon:9606"
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QY 469 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528	Query Match 17.8%; Score 295; DB 29; Length 1721; Best Local Similarity 49.0%; Pred. No. 3e-56; Matches 553; Conservative 0; Mismatches 567; Indels 9; Gaps 3;	/ol_gant.mus="pus muscutus" /mol_type="genomic_DNA" /db_xref="taxon:10090" <li1721 gene="GPRK5" locus_tag="HCM2438" origin<="" th=""><th>COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers source 1. 1721</th><th>AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Iu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. TITLE Direct Submission JOURNAL Submitted (16-NOY-2003) Celera Genomics, 45 West Gude Drive,</th><th></th><th>stazoa; Chordata; Craniata; Vertebr heria; Rodentia; Sciurognathi; Mur co 1721) Slanowski,S., Nielson,R., Thomas,P.</th><th></th><th>Db 662 CTGGTGGGCTCGGCTGCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCA 721 Qy 1179 TTACAAGGAAAAGGTCA 1195 </th><th></th><th>Qy 939 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCCGGCAACTGCAGGTTATC 998 . </th><th>Qy 879 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTCCACCTCCATGAACTCGGCATCGT 938 </th></li1721>	COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers source 1. 1721	AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Iu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. TITLE Direct Submission JOURNAL Submitted (16-NOY-2003) Celera Genomics, 45 West Gude Drive,		stazoa; Chordata; Craniata; Vertebr heria; Rodentia; Sciurognathi; Mur co 1721) Slanowski,S., Nielson,R., Thomas,P.		Db 662 CTGGTGGGCTCGGCTGCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCA 721 Qy 1179 TTACAAGGAAAAGGTCA 1195		Qy 939 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCCGGCAACTGCAGGTTATC 998 .	Qy 879 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTCCACCTCCATGAACTCGGCATCGT 938
L546 GCAIGSCAGGAAGTTATAGAAACGGGACTGTTTGAGGAACTGAATG 1594	1486 1416		Qy 1309 CAACGCTTAGGAAGCAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAA 1365	Db 1119 AAGGTTAAGCGGGAAGAGACTCTTGCAACACTGAGGTCAAATTCCAGCAT 1248 Qy 1249 GATAACTTCACAGAGGAAGAGACTATTTCCAGGAGTTAAATTCC 1308	1002 1129 1059	OY 1069 ATGGCTCCTGAGATCCTAATGGAAAAAGGTAATCCTATCCTGTGGACTGGCTTGCC 1128	989 TCGGC 822 GCAGC 949 ATGAA 882 CTAAA	OY 769 GCCTTFGAGACCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAGTGAG	582 709 642	Db 462 CÄGTĞĞĀĀTGGTTĀĞĀAĀGINININININININININININININININININININ	Db 402 TACTTGAAGGGAGACCCCTTCCACGAGTACCTGGATAGCATGTATTTTGACCGTTTTCTG 461 Qy 529 CAGTGGAAACTCTTCGAGAGTGCAACCAGTGTCAGAGTACTTCACTGAGTTCAGAGTG 588

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AGENCOURT 10181837 NIH MGC 101 Homo
IMAGE:6536408 5', mRNA sequence.
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plate: LLCM2697 row: 1 column: 08
High quality sequence stop: 640.
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Tissue Procurement: ATCC
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Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                    CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
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TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 708
                                                                                                                                                                   CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGTAAAATG
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_101"
/clone_Torgan: lung; "Vector: pOTB7; Site_1: EcoR1; Site_2:
/note="Organ: lung; "Vector: pOTB7; Site_1: EcoR1; Site_2:
/note="Organ and by oligo-dT priming. Directionally cloned
into EcoRJ(XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory. of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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mol_type="mRNA"
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Pred. No. 2.2e-53;
0; Mismatches 269;
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BU146436.1 GI:22659968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENCOURT 8728162 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:63391265', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU146436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates;
1 (bases 1 to 903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGGCIGIGAAGAICCCCGAGGGAGACCIGAICCGCGGNCGGGTGGGCACTGTTGGCTAC 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGCTCCAGAGGTCC---TGAAACACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC
                                                                                                                                                                                                                                                                                                                   .ate: LLCM2533 row: h column: 07
                                                                                                                                                                                                                                                                                           quality sequence stop: 635.
/lab hoSt="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNn made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                                               tissue_type="neuroblastoma, cell line"
                                                                                                                                                                                                     organism="Homo sapiens"

mol_type="mRNA"
                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                                                                                           clone="IMAGE: 6339126"
                                                                                                                                                                                   db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                903 bp
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ORIGIN

Query Match

Local

93

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Matches 455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1009 спесссопсався памесет с представления при при представляющим представления представляющим п
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 TICTIGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528
                                                                                                                                              BM794145
K-EST0075316 S22SNU16n1
5', mRNA sequence.
                                                       BM794145
BM794145.1 GI:19142377
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGGGGCCTTGTTTTAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTTCCACATCTACAACGTGGGCACGCGTGGCCCTGGACATGAGCCGGGTGATCTTTTAC 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATGAATGGGGGGTGACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAATGAGAAGCÁGATCCTCGÁGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAGGTGGCGAGAAGATGGCT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG
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                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  816
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                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
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                                                                       886 TACTCGGCCCAGATAGCCTGTGGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 АЛСТАТСССТСТААСААСТССАСААСААСАССТСВАССААСААСААСАТС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 GTGCTGGGGAAAGGTGGTTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAG 645
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1 (Dases 1 to 560)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 37 row: D column: 08
High quality sequence stop: 560.
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Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470
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/clone_lib="S22SNU16n1"
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/db_xref="taxon:9606"
/clone="S22SNU16n1-37-D08"
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/cell_line="SNU-16"
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UI-E-DXO-agn-o-23-0-UI.rl UI-E-DXO Homo sapiens cDNA
UI-E-DXO-agn-o-23-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coordinated Laboratory for Computational Genomics
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was lighted to an EcoR I adaptor, digested with Not I, and cloned directionally into pTTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCAAGA. This library was created for the program, Gene Discovery in the Visual system, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                                                                                                                 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UT-E-DXO is a cDNA library containing the following tissue(s): fetal eyes. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, according to Bonaldo, Lennon and Soares, Genome Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="UI-E-DX0-agn-o-23-0-UI"
/tissue_type="fetal eyes"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/mol_type="mRNA"
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 TACATGGCTCCGGAGGTGGTGAAGAA 566
                                                                                                                                   GACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACCACCCCCCATCTCTGACCTG
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                               TACATGGCTCCTGAGATCCTAATGGA 1091
                                                                GGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16,4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 272.2; DB 12; Pred. No. 2.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                        480
                                                                                                                                                                                                         420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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REFERENCE AUTHORS TITLE COMMENT JOURNAI Unpublished (1999)

RESULT 14 BQ061150

DEFINITION rocus

1017 bp
AGENCOURT 6862973 NIH MGC 99 Homo
5', mRNA sequence.
BOOKITE

sapiens cDNA clone IMAGE:5920182

mRNA

linear

EST 02-APR-2002

ACCESSION

BQ061150

VERSION KEYWORDS SOURCE FEATURES ORGANISM NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1017) BQ061150.1 GI:19884936 EST. Homo sapiens found through the I.M.A.G.E. http://image.llnl.gov Tissue Procurement: Lou Staudt Email: cgapbs-r@mail.nih.gov Contact: Robert Strausberg, Ph.D. Homo sapiens (human) Plate: LLCM2083 row: h column: 07 cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can quality sequence stop: 697.
Location/Qualifiers Consortium/LLNL at:

source

ORIGIN

Matches 526; Query Match

764

ب

Buteleostomi;

EST 17-DEC-1999

834

61

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Local Similarity
        1421 ACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGG 1480
                                                                                                                                                                                                                                               1304 CAGAGCAACGCTTAGGAAGCAGAGAAA---GTCTGATGATCCCAGGAAACATCATTTCT 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 TGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGG
                                                                                        TTAAAACGATCAACTITCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAG 1420
                                                                                                                                                                                           CGAAGCAGAGGCTGGGCTGCCAGGAGGAGGAGGGGGGGGTGCAGAGGTCAAGAGACACCCCTTCT 654
                                                                                                                                                                                                                                                                                                   ACTCCCACAAGTTCTCCGAGGAGGCCAAGTCCCATCTGCAAGATGCTGCTCACGAAAGATG 594
                                                                                                                                                                                                                                                                                                                                                     AGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAAC 1303
                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGAAGGTGAAGCGGGAGGAGGTGGACCGGCCGGGTCCTGGAGACGGAGG---AGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTACATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGT 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGGAACTGCAGGTTATCTGACC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATC 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTATGCCTTTGAGAGCCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAG 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGAGCCGGGCCTTGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTATGCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="PHIDM (phage-resistant)"
/clone lib="NIH MGC 99"
/clone lib="NIH MGC 99"
/clone lib="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="lymphoma, cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="IMAGE:5920182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 272.2; DB 13; Length 1017; Pred. No. 3.7e-51; 0; Mismatches 359; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI934968/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
           591
                                                                                                              651
                                                                                                                                                               529
                                                                                                                                                                                                                   711
                                                                                                                                                                                                                                                                        469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1541 CTATAGCATGGCAGGAAGAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1481 GGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTC
                                                                                                                                                                                                                                                                                                                         439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           715 ACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGGTGAAG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1030 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1934968 815 bp mRNA linear ES' wd17a07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2328372 3' similar to gb:L15388 G PROTEIN-COUPLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI934968.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINASE GRK5 (HUMAN);, mRNA sequence
                                 CTGGGGAAAGGTGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG
                                                                                                                                               CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
                                                                                                                                                                                                        TACTTGAGGGGAGAACCATCCCCACGAATATCTGGACAGCATGTTTTNTGACCGCTTTCTC
                                                                                                                                                                                                                                                       TICTIGCAAGAGCAGCCCTITAAGGATITCGTGACCAGCGCCTICTACGACAAGTITCTG 528
CTAGGAAAAGGGGGCTTCGGGTAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTANAATG
                                                                                                CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAANACACTTTCAGGCAGTATCGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCCCATGNGCAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAACG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGCTCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 815)
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone lib="Soares NFL T GBC S1"
/Clone lib="Soares NFL T GBC S1"
/Clone Torgan: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
                                                                                                                                                                                                                                                                                                                                                                                                                                               from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by B Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:2328372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:5673838
                                                                                                                                                                                                                                                                                                                                            16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type="mRNA"
                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                              Score 270.6; DB 9
Pred. No. 7.5e-51;
0; Mismatches 263
                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN-COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subtraction by Bento
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                  Length
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241 944 181 884 121

	4 CTTGCCTGCCTCATCTATGAGATGATCGAGGCCAGTCGCCGTTC 10	Db 54	U
) ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTC 1173	Qy 1129	Ø
	ATGGCTCCAGAGGTCCTGAACAACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 55	Db 111	D
28	ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1128	Qy 1069	iQ.
N	TTGGCTGTGAAGATCCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC 112	Db 171	Ο.
88	CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1068	2y 1009	Ų
Ü	. CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 172	Db 231	2
8	ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1008	2y 949	Ŋ
	GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 232	b 291	岁
_	TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948	у 889	×
	AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGGGGGCCTTGTTTAT 292	ь 351	岁
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	TATGCCTGCAAGCGCTTGGAGAAGAAGAAGAGGATCANAAAGAGGAAAAGGGGAGTCCATGGCC 472	531	ŏ
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Search completed: August 13, 2004, 18:41:51 Job time : 2909.87 secs

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	Sequence 4, Appli	TAME OF SHIPPING	Semience 10 Mm	Sequence 6. Appli	Sequence 24, Appl	Sequence 48, Appl	Sequence 12, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 8, Appli	Sequence 10, Appl	Sequence 68, Appl	Patent No. 5266464	Sequence 9, Appli	pedrence 2, White	Trada o Trada	Sequence 9 Appli			Sequence 11, Appl

APPLICANT: Walke, D. Wade APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc TITLE OF INVENTION: Encoding the Same FILE REFERENCE: LEX-0147-USA CURRENT APPLICATION NUMBER: US/09/802,117 CURRENT FILING DATE: 2001-03-08 PRIOR APPLICATION NUMBER: US 60/188,449 PRIOR APPLICATION NUMBER: US 60/188,449 PRIOR FILING DATE: 2000-03-10 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0 TYPE: DNA ORGANISM: homo sapiens 99.8%; Similarity 99.9%; 0; Mismatches Score 1655.8; Pred. No. 0; DB 4; Length 2249;

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CURRENT APPLICATION NUMBER: US/09/802,117
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 60/188,449
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1662
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Patent No. 6444456
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Best Local Similarity 99.8%;
Matches 1656; Conservative
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
FILE REFERENCE: LEX-0147-USA
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Qy 481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAAACTC		1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGGTGGAATTTGATGACAAA 1500
Qy 421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG		1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
Qy 361 AACCCGCAACCCTTCCTCAGCCAGGCCGCGCGACGAGTGCGAGGCGAGCAGCCACCTGAG	<u></u>	1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
Qy 301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCGACTTGTGGGAGTGCCCCTGCCCGGGG		1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
Qy 241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGGTGGCCGAGGAGGACGCCCC		1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
Qy 181 GAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC		1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
QY 121 GGGCTGCAGGGCTGCGCGGAAGCTCCGCCAGAACCTGTCCACAGCCTGTGT 180		1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
OY 61 AAGCCCTCGGACTGCGACAAGCAGCAAAGAGCTGGAGGGGGGGG		1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
Qy 1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCTAACACCGCCTACCTGCAGGCCCGG		961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
Query Match 99.7%; Score 1654.2; DB 4; Length 1662; Best Local Similarity 99.8%; Pred. No. 0; Matches 1656; Conservative 0; Mismatches 3; Indels 0;		901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATGTCTATCGGGACATGAAGCCTGAG 960
; DEMOST: 1062 ; TYPE: DNA ; ORGANISM: Human US-09-738-894A-1		841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LEVER 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
TITLE OF INVENTION: HOLD FOUNDAMENT HUMAN KIND FILE REFERENCE: CL000636 CURRENT APPLICATION NUMBER: US/09/738,894A		721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
GENERAL INFORMATION: GENERAL INFORMATION: GUEGLER, Karl et al FITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC FITLE OF INVENTION: ACT ACT FOR THE PROPERTY THROUGH THE PROPERTY OF THE PROPERTY		661 AAACTGGACAAGAAGCGGCTGAAGAAGAAGATGGCGAGAAGATGGCTCTCTTGGAAAAG 720
RESULT 3 US-09-738-894A-1 Sequence 1, Application US/09738894A		601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
Oy 1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659		541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
1561		481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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                    GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
                                                                                               ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG
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Best Local Similarity 99.8%;
Matches 1656; Conservative
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Sequence 1, Application US/09964469

Patent No. 6579709

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

ITILE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND

ITILE OF INVENTION: THEREOF

FILE REFERENCE: CL000636DIV

CURRENT APPLICATION NUMBER: US/09/964,469

CURRENT ELING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: 60/208,331

PRIOR APPLICATION NUMBER: 09/738,894

PRIOR APPLICATION NUMBER: 09/738,894

PRIOR FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 1662
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                                                                            ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG
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RESULT 5 US-09-802-117-3

; Sequence 3, Application US/09802117

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; TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/09/802,117
CURRENT APPLICATION NUMBER: US 60/188,449
PRIOR APPLICATION NUMBER: US 60/188,449
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 5
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Best Local Similarity 99.8%;
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GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC
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                                AAACTGGACAAGAAGCGGCTGAAGAAGAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG
                                                   AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTTGGAAAAG
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Pred. No. 5.3e-249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.2%;
Best Local Similarity 96.8%;
Matches 630; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL000636
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GUEGLER, KAYÎ et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
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                                           CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375
                                                               CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCC
                                                                                                                       GAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315
                                                                                                                                                          GAGCAGCAGCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 617.4; DB 4;
Pred. No. 2.2e-142;
0; Mismatches 21;
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US-09-964-469-3
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APPLICANT: GUEGLER, KArl et al
APPLICANT: GUEGLER, KARl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOOGSGUT
CURRENT APPLICATION NUMBER: US/09/964,469
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR APPLICATION NUMBER: 0907-08-01
PRIOR APPLICATION NUMBER: 091/738,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORCANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Applic
Patent No. 6579709
                                                                                                                                                                                                                                                                                                                                                            Matches 630;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                  GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
                                                                                                                                                                                                        AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGCGTAGCCTGGCCCTGCCC
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      CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC
                                                                  GAGCAGCAGCATCGGTCGCCGCCTCTTCCGTGACTTCCCTAGCCACAGTGCCCACGTTC
                                                                                                                         GGGCTGCAGGGCTGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT
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Pred. No. 2.2e-142;
0; Mismatches 21;
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RESULT 8
US-08-464-954A-2
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Patent No. 6255069
                                                                                                                                                     FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,084
FILING DATE: June 11, 1993
ATTORNBY/ACENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JEFF-0118
TELECOMMUNICATION INFORMATION:
                                                                                                      TELEFAX: (609) 779-8488 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TITLE OF INVENTION: K
TITLE OF INVENTION: K
                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI, APPLICANT: PRIYA
TOPOLOGY:
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                                                   TYPE: N
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CITY: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jane Massey Licata, Esq. STREET: Woodland Falls Corporate Park STREET: 210 Lake Drive East, Suite 201
                                  STRANDEDNESS:
                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
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                                                                      2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
LINEAR
NO
                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PS/2
                                                                                                                                          (609) 779-2400
                                   SINGLE
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 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG
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RESULT 9
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PRILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/123
APPLICATION NUMBER: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: NO. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
FEATURE:
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Pred. No. 1.1e-93;
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RESULT 10
US-08-454-439-12
                                                                                                                                                                                               Sequence 12, Application Patent No. 5591618
                                                                                                                                                                            GENERAL INFORMATION:
                                                            APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                       CORRESPONDENCE
                                            NUMBER OF SEQUENCES:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Chicago CITY: Chicago Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/1:
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: No. 5591618and, Greta REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 30-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 31-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 25.2%;
Local Similarity 56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GECCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGGAAGCCCTCGGACTG 74
                                                               CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                                                                                                                                                                                                    CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG
                                                                                                                                                                                                                                              AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG
                                                                                                                                                                                                                                                                                               CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                            GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448
                                                                                                                                                          CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC
                                                                                                                TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 418.2; DB 1;
Pred. No. 1.1e-93;
0; Mismatches 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31981
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                                                 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT
                                                                                                      TGAAATTGATGATTTCTCTGAGGTTCGGGGGGGGGGATTTGATGACAAAGATAAGCAGTT 1511
                                                                                                                                                                                                                                                                                                                  GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
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                                                                                                                                                          TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463
                                                                                                                                                                                                            TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
                                                                                                                                                                                                                                                                   TGCCCGCGAGGTGAAGGAGCACCCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGCTGGTGAAGGAGGTCCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283
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                                                                                                                 Matches
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                      FEATURE:
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LOCATION:
                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                           STRANDEDNESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
                                                                                                                                                                                                                                                  TOPOLOGY:
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                           CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                                                                                   GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCCTCGGACTG
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Pred. No. 1.1e-93;
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GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
                                                                                         GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGAICTGAA 1211
                                                                                                                                                           GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTGTACGAGAT
                                                                                                                                                                                                    AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 115:
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                                                      GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA
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CGAGTGCTTCCAAGAGCTGAATGTC 1608
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                                          GGGACTGTTTGAGGAACTGAATGAC 1596
                                                                                  CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583
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RESULT 12
US-08-221-817-21
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                                                             TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/123
APPLICATION NUMBER: 10/123
PTITING DATE: 17 SEP 1993
                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/221,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                              SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pair
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                     TELECOMMUNICATION INFORMATION:
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CITY: Ch
STATE: I
COUNTRY:
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                   TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                      REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
STRANDEDNESS:
                  TYPE:
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Best Local Similarity
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Pred. No. 3.5e-88;
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                                                                                                                                                                                                                                                                                      Patent No. 5591618
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                Sequence 21,
                                                                                                                                                                                             NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A NO. 5591618el G
TITLE OF INVENTION: Kinase GRK6
                                                                                                                              STATE:
                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Borun
                                                                                                                  COUNTRY:
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           US/08/454,439
                                                                                                                                                         233
                                                                                                                                                         South
                                   Version
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAAGGTCAGTAAAGAGGATCTGAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein-Coupled Receptor
                                                                                                             #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1505
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CLASSIFICATION:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,81
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312) 474-04-
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
            GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
                                                                                                                             ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
                                                                                                                                                                                                                        GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
                                                                                                                                                                                                                                                                      ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG
                                                                                                                                                                                                                                                                                                                                                                  AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                               CTTCCTCAGGCCAGGCCGTGGCCAACCAAGTGCCAACCACCACTGAGGAAGAGCGAGT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGCTGCAGGGGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATTGGGCCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATCGTAAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCCACATCAGCCA 134
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                                                                                      GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA
                                                                                                                                                                                                                                                                                                                 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCCTTTAA 491
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RESULT 14
PCT-US94-10487-21
; Sequence 21, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; APPLICANT: ICOS Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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NAME/KEY: LOCATION:

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Best Local Similarity Matches 876; Conserv

Query Match Best Local

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PCT-US94-10487-21
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: NOLAND, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OCCUMANTE. Data T. Data T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 17 SEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marun
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  TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445
                                           TOGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTATGCCAAAGACACTCGC 1451
                                                                                                             TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385
                                                                                                                                                                    GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTGCGGGACAGTCGCCCTTCCAGCAGAAGAAGAAGAAGATCAAGCGGGAGGAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGGGGGCGCTAGGCTGCCTCCTGTACGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCCTGTGCATGTTCCTGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCCGTGGAGATGAAGGGTGG 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCCTTGTCATGAGCCTGATGAATGGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
                                                                                                                                                                                                                           ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGGTGTCGTGGAGGTGG 1325
                                                                                                                                                                                                                                                                                                                                      GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCCACAGGCACGCTC 1265
                                                                                                                                                                                                                                                                                                                                                                                          GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCCAAGACCCATCT 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGGAAATCTTGGA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
                                                                                                                                                                                                                                                                               AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGCTGGCTTTCCCGAAGCACGTGCTGTTGTTCTATGCTGCCGAGATCTGCTGTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAACGAATAAAGAAGCGGAAGGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTTGGGGA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCICITCCAGGAGCIGACCCGGCIGACCCATGAGTACCTAAGCATGGGC--CCTTTIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG
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Query M Best Lo Matches Qy	US-08-	RESULT US-08-2 Seque Pateu Pateu AI AI III V CC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Query Match 23.5%; Score 389.4; DB 1; Length 2206; Best Local Similarity 55.3%; Pred. No. 1.4e-86; Matches 866; Conservative 0; Mismatches 681; Indels 18; Gaps 5; 15 GGCCCTGGACAACCTGAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74	OPERATING STITEM: COMPAINEDS SOFTWARE: PATENTIA Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/221,817 FILING DATE: CLASSIFICATION 1435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/123,932 FILING DATE: 17 SEP 1993 ATTORNEY/AGENT INFORMATION: NAME: No. 5532151and, Greta E. REGISTRATION NUMBER: 31,302 REFERENCE/DOCKET NUMBER: 31981 TELECOMOUNICATION INFORMATION: TELEPHONE: (312) 474-0448 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 2206 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE: NAME/KEY: CDS LOCATION: 311926	pplicatio 2151 2151 Chantry Gray, Pa Gray, Pa Hoekstra VENTION: EQUENCES: EQUENCES: EQUENCES: EQUENCES: EQUENCES: I BOTUN 6300 Seat 11inois USA 06 ADABLE FOR PE: Flor	1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
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AAA 	612 GGTATGTGCCGTCCAGGTGAAAACACTGGGAAGATGTATGCCTGAAGAAACTGGACAA 671	273 CGCCTTCCTGGATGGGCCGGCCCGGGTATGAGTGACCCGGGATGACAAGCCGGAAGCCATĠ 332 312 CGCCTGCCGGGGTGGGCACTTGTGGAGTGACCCGGATGACAAGCCGGAAGCCAACC 371	75 CGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131

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	1569 AACGG 1573	¥
1580	1521 CTTCTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGA 1	ъ
1568	1509 GTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGA 19	γ
1520	1461 TCTGGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGA 1	ъ
1508	1449 CGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCA 19	Σγ
1460	1401 AGCTGGCATGCTGGAGCCGTTCAAGCCTGACCCCAGGCCATTTACTGCAAGGATGT 1	Ъ
1448	1389 AGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACAT 1	Σγ
1400	1341 CAGTGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGG 1	ď
1388	1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGA 1:	γ
1340	1281 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACCGACCCTGGGGTGTCGTGGGGG 1:	В
331	1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331	βy
1280	1221 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1:	рb
271	1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271	Ş
220	1161 GATCGCAGGCCAGTCGCCCTTCCAGCAGAAGAAAAAAAAA	οb

Search completed: August 13, 2004, 18:45:37 Job time: 91.4555 secs